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Q961k8 drosophila
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Q8aww5 gallus gall
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ALIGNMENTS

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RESULT
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   A TO CONTRACT TO THE PROPERTY OF THE PROPERTY 
               TISSUE-Melanoma;
TISSUE-Melanoma;
Mitchell M.S., Kan-Mitchell J., Minev B.,
"Identification of a novel melanoma gene (
"Identification of a novel melanoma gene (
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01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
MYELOBLAST KIAA0230 (Fragment).
                                                                                                                                                                                                                                   Genomics
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KIAAO230.
Homo sapiens (Human).
Homo sapiens (Human).
Tharvota; Metazoa; Chordata; Metazoa; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Melanoma; PubMed=7959781; MEDLINE=95048383; PubMed=7959781; Weiler S.R., Taylor S.M., Deans R
IL-1 receptor antagonist -
cytolytic T lymphocytes.";
                                                                                                                                                                                                                                                          "Assignment of a human melanoma associated gene MG50 (D2S448) to chromosome 2p25.3 by fluorescence in situ hybridization."; Genomics 22:243-244(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Bone marrow;
MEDLINE=97191544; PubMed=9039502;
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                                   , Edman C., Deans R.J.;
(MG50) - likely the gene for
epitopes recognized by human
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Pfam; PF00047; ig; 4
Pfam; PF000560; LRR; 5
Pfam; PF001463; LRRCT; 1.
Pfam; PF001463; Vwc; 1.
Pfam; PF00093; Vwc; 1.
PFRINTS; PR00457; ANPEROXIDASE.
SMART; SM00408; IGC2; 4
SMART; SM00082; LRRCT; 1.
SMART; SM00013; LRRCT; 1.
SMART; SM00316; LRR TYP; 4
SMART; SM00214; VWC; 1.
SMART; SM00214; VWC; 1.
                                  Strausberg R;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ
EMBL; BC009496; AAH09496.1; -.
InterPro; IPR002007; Anim_peroxidase.
InterPro; IPR001007; VWF_C.
Pfam; PF03099; An.peroxidase; 1.
Pfam; PF00093; VWC; 1.
SMART; SM00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                Q96GF5 PRELIMINARY; PRT; 221 AA.
Q96GF5;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein (Fragment).
Homo Sapiens (Human).
Hypothetical NON_TER
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Mammalia; Eutheria;
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983; BAA13219.1; -.
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Q96LH9 PRELIMINARY; PRT;
Q96LH9; O1-EC-2001 (TrEMBLrel. 19, Created
01-DEC-2001 (TrEMBLrel. 19, Last sc
01-MAR-2003 (TrEMBLrel. 23, Last ar
Hypothetical protein FLJ25471.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Crani
Mammalia; Eutheria; Primates; Catal
NCBI_TaxID=9606;
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01-JUN-2001
01-JUN-2001
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Rattus norvegicus (Rat).
Rattus norvegicus (Cat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Sprague-Dawley;
Long X., Bigsby R.M., Rephew K.P.;
Long X., Bigsby R.M., Rephew K.P.;
"Rat gene similar to human melanoma-associated
submitted (FEB-2001) to the EMBL/GenBank/DDBJ of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2002 (TrEMBLrel. 21,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (FEB-2001) to the EMBL; AF346790; AAK30128.1;
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102; Conserv
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175; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPRVDLRVWQDCCEDCRTRGQFNAFSYHFRGRRSLEFSYQEDKPTKKTRPRKIPSVGRQG
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                                                                                                                                                                                                                                                                                                             --QSVWMTVVNPRQQHEVGKRQMPVCECKNGQVTCFVEACHLQPAAA---
                                                                                                                                                                                                                                                                                                                                                                                          EHLSNSTSAFSTRSDASGTNDFREFVLEMQKTITDLRTQIKKLESRLSTTECVDAGGESH 120
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224 AA;
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Pred. No. 7.
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2; Mismatches
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                           Craniata; Vertebrata; Catarrhini; Hominidae,
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Sciurognathi; Muridae;
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                                            Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., Georg
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall
Nunco J., Pacleb J., Parágas V., Park S., Phouanenavong S.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY051536; AAK92960.1; -.
E1yBase; FBgn0011828; Pxn.
InterPro; IPR007110; Ig-like.
InterPro; IPR00710; Ig-like.
InterPro; IPR00710; Ig-C2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001
01-DEC-2001
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                         InterPro;
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PF02345;
PF00093;
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     IPR003006;
IPR001007;
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RA Adams M.D.; Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Adams M.D.; Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenorort L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenorort L.B., Davies P.,
RA Ge Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Ge Pablos B., Delcher A., Bounes M., Dugan-Rocha S., Dukov B.C., Dunn P.,
RA Ge Pablos B., Delcher A., Boynes M., Dugan-Rocha S., Dukov B.C., Dunn P.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
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01-MAY-2000
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SMART; SM000214; VWC; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS01208; VWFC; 1.
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Pfam;
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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RESULT 7
Q91BG7
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AC Q91E
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OC Euka
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Best Local
                                                                            091BG7;
01-OCT-2000
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng J., Zheng J
  Eukaryota;
                                         Kielin.
                                                                                                                                       Q91BG7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00408; IGC2; 3.
SMART; SM00013; LRRNT; 1.
SMART; SM00369; LRR_TYP; 3.
SMART; SM00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE003475; HSSP; P05164; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshre Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nel Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reinert K., Remington K., Saunders R.D.C., Scheeler F., S
                                                            01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunoglobulin
SEQUENCE 1527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FlyBase; FBgn0011828; Pxn.
InterPro; IPR002007; Anim_peroxidase.
                      Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ?fam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF01462; LRRNT;
PF00093; vwc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS50835; IG_LIKE; 4.
PS50506; LRR_TYPICAL; 1.
PS01208; VWFC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                    ATAESYDSPLESLYDVNEERVSGLEELIGSFQKELKKLHKKLRKLEDSCNSADSEPVAQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INLYLWQEC-----GRCNSPPAIFD-----SYIPQTYTKRSNRQK-RDLGKENDEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VDLRVWQDCCEDCRTRGQFNAFSYHFRGRRSLEFSYQEDKPTKKTRPRKIPSVGRQGEHL
                                                                                                                                                                                                                                                                                                                                                                                                                                              SNSTSAFSTRSDASGTNDFR----EFVLEMQKTITDLRTQIKKLE--
                                                                                                                                                                                                                                           PPGVDPLTPPEACCPHC 1523
                                                                                                                                                                                                                                                                                  ---AVPVNIPGACCPVC
                                                                                                                                                                                                                                                                                                                          VQLAAAPPQLVSKPKRSHCVDDKGTTRLNNEVWSPDVCTKCNCFHGQVNCLRERCGEVSC
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IPR001007;
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IPR003598;
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  Metazoa;
                                                        ) (TrEMBLrel.) (TrEMBLrel.) (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                         PRELIMINARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                An_peroxidase; 1.
ig; 4.
LRR; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              domain.
                    (African
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
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  Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.3%;
                                                                                                                                                                                                                                                                                                                                                             SRLSTTECYDAGGESHANNTKWKKDACTICECKDGQVTCFVEACPPATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRR_typ.
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Ig_c2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170513 MW;
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                    clawed
                                                          15,
15,
23,
                                                                                                                                                                                                                                                                                  167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27;
                                                        Created)
Last sequence up
Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 186; DB 5; Pred. No. 4.5e-09;
Craniata;
                                                                                                                                         PRT;
                  frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                         2327
  Vertebrata;
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                                                                               update)
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                                                        update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Moshrefi A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pacleb J.M.,
  Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48;
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RESULT 8
Q8AWW5
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Best Local S
Matches 48
                                                                                                                                                                                           Q8AWW5;
Q8AWW5;
Q1-MAR-2003
Q1-MAR-2003
Q1-MAR-2003
                                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, Cysteine-rich motorneuron 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                          SEQUENCE FROM N.A. MEDLINE-22395914; PubMed-12508231; Kolle G., Jansen A., Yamada T., Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00210; TSPN; 1.
SMART; SM00214; VWC; 27.
SMART; SM00216; VWD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00093; vwc; 22. Pfam; PF00094; vwd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matsui M., Mizuseki K., Nakatani J., Nakanishi S., Sasai Y., "Xenopus Kielin: A dorsalizing factor containing multiple chordin-type repeats secreted from the embryonic midline."; proc. Natl. Acad. Sci. U.S.A. 97:5291-5296(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE-Embryonic floor plate;
MEDLINE-20266358; PubMed-10779551;
                                                                                                                                               Eukaryota;
                                                                                                                                                         Gallus gallus (Chicken).
                                                                                                                                                                      CRIM1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam;
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NCBI_TaxID=8355;
  SEQUENCE
                EMBL;
                           Dev. Dyn.
                                      cord.
                                                                                                                                 Archosauria; Aves;
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                                                 "In ovo electroporation
                                                                                                           NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                            146
                                                                                                                                                                                                                                                                                                                                                                         119
                                                                                                                                                                                                                                                                                                                                                                                                                                               239
                                                                                                                                                                                                                                                                                                    407
                                                                                                                                                                                                                                                                                                                                                                                                290 PAQLLAKDDR--LQRLEEAVKGLTNMIDMIKSQNADLQARVIALESCECRRSTCVWEDKE
AY098584; AAM:
NCE 1048 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P56682;
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                                                                                                                                                                                                                                                                                                                                                                                                                       67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF01826;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 RVWQDCCEDCRTRGQFNAFSYHFRGRRSLEFSYQEDKPTKKTRPRKIPSVGRQGEHLSNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS01186; EGF_2; 1. PS01208; VWFC; 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; IPR006209; EGF_like.
; IPR002919; TIL_Cysrich.
; IPR003129; TSPN.
; IPR001007; VWF_C.
; IPR001846; VWF_D.
                                                                                                                                                                                                                                                                                                                                                                                                                                            RPWH-----CENRSDSLPLPYSLSGERQME----DEEIQREPRAPDLSDTDHYQQQQSEV 289
                                                                                                                                                                                                                                                                                                    QSGEVSCTPKLCPPVTCSDPVTLPNECCPLC
                                                                                                                                                                                                                                                                                                                                                  YQDSET-WKKDACNICVCVGGSVTCSVRKDWPQCLGCFHEGRNYNNKDIFSVGPCMSCIC
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                                                                                                                                                                                                                                                                                                                                                                                                                      TSAFSTRSDASGINDFREEVLEMOKTITDLRTQIKKLESRLSTTE---
                           226:107-111(2003).
                                                                                                                                               Metazoa;
                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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              AAM28339.1
                                                                                                                                                                                                                                                                                                                           -EACPPATCAVPVNIPGACCPVC 167
                                                                                                                                  Neognathae;
                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.0%;
22.7%;
  114942 MW;
                                                 Yamada T., Lit
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                                                                                                                                                                                             Last sequence update)
Last annotation updat
                                                                                                                                                                                                                    Created)
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                                                           Little
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   25E4D82C40B08231 CRC64;
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                                                 developing
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                                                  chick spinal
                                                                                                                                  Phasianinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                       CVDAGGE
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RESULT
Q8BS96
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AC Q8
AC Q8
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Best Local (
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Q8BS96 PRELIMINARY;
Q8BS96;
01-MAR-2003 (TrEMBLrel. 23, C
01-MAR-2003 (TrEMBLrel. 23, L
01-MAR-2003 (TrEMBLrel. 23, L;
Cysteine-rich motor neuron 1,
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=20108580; PubMed=10642437;
Kolle G., Georgasl K., Holmes G.P., Little M.H., Yamao Kolle G., Georgasl K., Holmes G.P., Little M.H., Yamao McCRIMI, a novel gene encoding a cysteine-rich repeat "CRIMI, a novel gene encoding and implicated in vertebrat
                                                                                                                                                                                                                                                                                                                                                                                                                               Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 112-1036 FROM N.A.
SEQUENCE OF 112-1036 FROM N.A.
Kolle G., Georgas K., Holmes G.P., Little M.H., Yamada
Kolle G., a novel gene encoding a cysteine-rich repeat po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mech.
EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein,
Homo sapiens (Human),
Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Cysteine-rich repeat-containing protein S52 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9NZV1; Q9H318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00139; THIOL PROSITE; PS01208; VWFC;
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                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organogenesis.";
h. Dev. 90:181-193(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organogenesis
                                                                                                                                                                                                                                       823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dev. 0:0-0(2000).
AF167706; AAF34409.1;
AF168681; AAG37011.1;
P15358; 1SKZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 GESHANNTKWKKDACTICECKDGQVTCFVEACPPATCAVPVNIPGACCPVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00093; vwc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF02822; Antistasin; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SM00121; IB; 1
SM00214; VWC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HGNC:2359;
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                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                     GKAYADEERWDLDSCTHCYCLQGQTLCSTVSCPPLPCVEPINVEGSCCPMC
                                                                                                                                                                                                                                                                          GESHANNTKWKKDACTICECKDGQVTCFVEACPPATCAVPVNIPGACCPVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS00139; THIOL_PROTEASE_CYS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR004094; Antistasin.
IPR000867; Insl_gro_fac_pr.
IPR000169; SHprot_acsite.
IPR001007; VWF_C.
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1036
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                                                                                                                                                                                                                                                                                                                                                                                                         34 POTENTIAL
113737 MW; 10CBF
                                                                                                                                                                                                                                                                                                                                        16.6%;
43.1%;
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45.1%;
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                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                      Score 160; DB
Pred. No. 9.3e
11; Mismatches
                                                                                       Created)
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1; Mismatches
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                                                                                                                                 PRT;
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. No. 4.8e-07;
ismatches 17;
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.3e-07;
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                                                                                NON_TER
SIGNAL
SEQUENCE
                                                                                                                                                                                                                                                     "CRIM1, a novel gene encoding developmentally regulated and and organogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the RIKEN Genome Exploration Research "Analysis of the mouse transcriptome 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                              MEDIINE=20108580; PubMed=10642437; Kolle G., Georgasl K., Holmes G.P., Little M.H., "CRIM1, a novel gene encoding a cysteine-rich redevelopmentally regulated and implicated in vert
                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                         CRIM1
                                                                                                                                                                                                                                                                                                                                                                                            Cysteine-rich
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01-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                Signal.
                                                                                                                                              SMART;
                                                                                                                                                                             InterPro; IPR004094;
InterPro; IPR000867;
InterPro; IPR001007;
                                                                                                                                                                                                                                    EMBL;
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                                                                                                                           PROSITE;
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                                                                                                                                                                                                                                               Mech.
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                                                                                                                                                                     Pfam;
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                                                                                                                                    n; PF02822; Antistasin; 4
n; PF00093; vwc; 6.
RT; SM00121; IB; 1.
RT; SM00214; VWC; 6:
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814
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                                                                                                                                                                                                                                               Dev.
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22; Conserv
                                        Similarity
22; Conser
GKTYADEERWDIDSCTHCYCLQGQTLCSTVSCPPLPCAEPIKVEGSCCPMC
                   GESHANNTKWKKDACTICECKDGQVTCFVEACPPATCAVPVNIPGACCPVC
                                                                                                                           PS01208;
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                                                                                  1028
                                                                                                                                                                                                                                                                                                                               s (Mouse).
Metazoa; Chordata; C
Metazoa; Rodentia; C
                                                                                                                                                                                                                                             90:181-193(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     286 AA;
                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
ch repeat-containing protein CRIM1 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                 A,
                                                                                                                                                                                                              Crim1
                                                                                                                           WC; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                1
25 POT
113160 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32314 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.3%;
                                                                                                                                                                              Antistasin.
Insl_gro_fac_pr.
VWF_C.
                                                16.3%;
43.1%;
                                                                                                                           6
                                                                                                                                                                     4
                                       Score 157; DE
Pred. No. 1.8e
L1; Mismatches
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l; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Research
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                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; I
Sciurognathi; Muridae;
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                                                                                  743058AA481D5ED8
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                                   DB 11,
1.8e-06;
18;
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on functional
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                                                            Length 1028;
                                                                                  CRC64;
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                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         annotation
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864
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Best Local S
Matches 47
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PRINTS; PR00457; ANPEROXIDASE.
SMART; SM00408; IGC2; 3.
SMART; SM00013; LTRNT; 1.
SMART; SM00369; LTR_TYP; 2.
SMART; SM00214; VWC; 1.
 Q9IB91
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q23991;
                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 development."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEROXIDASIN precursor. PXN OR CG12002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBO J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Olson P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE-Salivary gland;
MEDLINE-94341255; PubMed-8062820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FlyBase; FBgn0011828; Pxn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nelson
                                                                                                                                                                                                                                                                                                                                                                                                                                                         [mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peroxidasin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          m; PF03098; An_peroxidase; 1.
m; PF00047; ig; 4.
n; PF00560; LRR; 5.
pF01462; ITT
                                                                               1505
                                                                                                                                              1445
                                                                                                                                                                                                              1385
                                                                                                                                                                                                                                                                             1345
                                                                                                              150
                                                                                                                                                                              105
                                                                                                                                                                                                                                             60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R.E., Fessler L.I., Takagi Y.,
P.F., Parker C.G., Fessler J.H.;
                                                                                                                                                                                                                                                                                                            4 VDLRVWQDCCEDCRTRGQFNA----FSYHFRGRRSLEFSYQEDKPTKKTRPRKIPSVGRQ
                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13:3438-3447(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS50835; IG_LIKE; 4.
PS50506; LRR_TYPICAL; 1.
obulin domain; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR007110;
IPR003598;
                                                                               EVSCPPGVDPLTASGGLLP
                                                                                                            PATC---AVPVNIPGACCP 165
                                                                                                                                              VAQVVQLAAAPPQLVSKPKRSHCVDDKGTTRLNNEVWSPDVCTKCNCFHGQVNCLRERCG
                                                                                                                                                                                                              NDEVATAESYDSPLESLYDVNEERVSGLEELIGSFQKELKKLHKKLRKLEDSCNSADSEP
                                                                                                                                                                                                                                           GEHLSNSTSAFSTRSDASGTNDFR----
                                                                                                                                                                                                                                                                             INLYLWQEC-----GRCNSPPAIFVPTYR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR000372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR002007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR001611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                         24 1535
1535 AA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel.
 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a novel
                                                                                                                                                                                                                                                                                                                                                          16.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig_c2.
Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LRR.
                                                                                                                                                                                                                                                                                                                                                                                                         171084 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anim_peroxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               enzyme-matrix protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01,
01,
23,
                                                                                                                                                                             SRLSTTECVDAGGESHANNTKWKKDACTICECKDGQVTCFVEACP
                                                                                                                                                                                                                                                                                                                                            27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                          Score 153.5;
Pred. No. 6.1
                                                                                                                                                                                                                                                                                                                                                                                                                        PEROXIDASIN
                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
 PRT;
                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         1B2D7A0C76339D64 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1535
 1447
                                                                                                                                                                                                                                           -EFVLEMQKTITDLRTQIKKLE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Blumberg
                                                                                                                                                                                                                                                                                                                                         5; DB 5;
5.1e-06;
hes 68;
 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA.
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B.
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                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Keene D.R.,
                                                                                                                                                                                                                                                                             KPT-PSGDRQKRDLGKE
                                                                                                                                                                                                                                                                                                                                                                           1535;
                                                                                                                                                                                                                                                                                                                                            57;
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                             1384
                                                                                                                                                                                                                                                                                                             59
                                                                                                                                                                                                                                           104
                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
Q9XSV8
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Query Match
Best Local S
Matches 27
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InterPro; IPR001007; VWF_C.
InterPro; IPR001007; VWF_C.
                                                                                                                                                                                                                                                                                                    Q9XSV8;
01-NOV-1999
01-NOV-1999
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collagen.
SEQUENCE
   InterPro;
InterPro;
                                            InterPro;
InterPro;
                                                                                         "Characterization of cattle submitted (MAR-1999) to the EMBL; AJ133488; CAB46239.1; HSSP; P56682; 1CCV.
                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
Bovidae; Bovinae; Bo
                                                                                                                                                                                                                                                                        SCO-spondin
SCO-SPONDIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pfam; PF01410; COLFI; 1.
pfam; PF01391; Collagen; 18.
pfam; PF00093; vwc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Type I collagen COL1A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9IB91;
01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00038; COLFI; 1.
SMART; SM00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom; PD000007; Collagen; 2.
ProDom; PD002078; Fib_collagen_C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. Goto T., Katada T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus laevis (African clawed Eukaryota; Metazoa; Chordata; C
                                                                                                                                                 Gobron S.,
                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                         Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopodinae; Xer
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amphibia; Batrachia;
                                  InterPro;
                                                                             InterPro;
                                                                                                                                                                                                NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104
                                                                                                                                                                                                                                                                                                                                                                                                                                      84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27;
); IPR005208; Cys_knot.

); IPR005207; Cys_knot_C.

); IPR001545; Gly_hormoneB.

); IPR002191; TIL_Cysrich.

); IPR001007; VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CPVCLQKRAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS01208; VWFC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                     CPVCTDNDAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EHDVQTSDCVQ-HGITYSNRDVWKPEDCQICVCDNGNILCDEVMCEDADCPNPVIVPGEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESRLSTTECVDAGGESHANNTKWKKDACTICECKDGQVTCFVEACPPATCAVPVNIPGAC
                                                                                                                                                    Creveaux
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1447 AA;
                                                                                                                                                                                                                                                                                                 (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                     (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alpha
                                                                                                                                                                                                               Bos
                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                      93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.9%;
38.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137446
                                                                                                                    Didier R., Meiniel R., ttle SCO-spondin."; the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                    12,
12,
23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15,
15,
22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence up
                                                                                                                                                                                                                                                                                                      Last sequence u
                                                                                                                                                                                                                                                                                                                                Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 152.5;
Pred. No. 7.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          frog).
Craniata; Vertebrata; Euteleostomi;
Craniata; Vertebrata; Pipidae;
                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A4A6DD2B4158E38B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No.
                                                                                                                                                                                                                                                                                                                                                              1637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
                                                                                                                                                                                                                                                                                                    update;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31;
                                                                                                                        databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                             Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1447;
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DR SQ
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Best Local S
Matches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8SPM4;
Q8SPM4;
Q1-JUN-2002;
Q1-JUN-2002;
Q1-MAR-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART;
SMART;
SMART;
SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS00261; GLYCO_HORMONE_BETA_1;
PROSITE; PS50092; TSP1; 11.
PROSITE; PS01208; TWFC; 1.
NON_TER 1 1
NON_TER 1 1
                                                                                                                                                                                                                      "Subcommissural organ/Reissner's fiber complex: characterization SCO-spondin, a glycoprotein with potent activity on neurite outgrowth.";
                                                                                                                                                                                                                                                                                                                                                                           Bos taurus (Bovine).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bumanmalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovinae; Bos.
                               Pfam;
Pfam;
                                                     Pfam;
                                                                                                                                                                                                 Glia 32:177-191(2000).
EMBL; AJ416457; CAC94914.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SCO-spondin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                 TISSUE=Subcommissural organ;
MEDLINE=20465125; PubMed=11008217;
                                                                  Pfam;
                                                                             Pfam;
                                                                                       InterPro;
                                                                                                   InterPro;
                                                                                                            InterPro;
                                                                                                                      InterPro;
                                                                                                                                  InterPro;
                                                                                                                                             InterPro;
                                                                                                                                                       InterPro;
                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                          Gobron S
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                              Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                           Meiniel A.;
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
FISSUE=Subcommissural organ;
                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9913;
                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15
                            n; PF00007; Cys_knot; 1.
n; PF00754; F5_F8_type_C; 1
n; PF00057; Idl_recept_a; 1
n; PF01826; TIL; 10.
m; PF00090; tsp_1; 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; PF01826; TIL; 3.
1; PF00090; TSP_1; 11.
17; SM00041; CT; 1.
17; SM00068; GHB; 1.
17; SM00209; TSP1; 11.
17; SM00214; VWC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174 EKP 176
          PF00094; vwd; sm00041; CT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity 42.9
27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQP 1540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GRPHPPGSEWQK-ACESCRCVSGESIC-TQHCPPLTCAQGETAVQEPGGCCPTCRQEAPE 1537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GESHANNTKWKKDACTICECKDGQVTCFVEACPPATCA---VPVNIPGACCPVCLQXRAE 173
                                                                                                                                            IPR000421;
IPR001545;
                                                                                                                                                                16457; CAC94914.1; -.
IPR001064; Crystallin.
IPR006208; Cys_knot.
IPR006207; Cys_knot_C.
                                                                                       IPR001846;
                                                                                                                         IPR002919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1637 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 21, Created)
(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 23, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173347 MW;
                                                                                      VWF_D.
                                                                                                                      TIL_Cysrich.
                                                                                                                                         Gly_hormoneB
                                                                                                                                LDL_receptor_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 143.5; DB 6;
Pred. No. 6.1e-05;
7; Mismatches 24;
                                                     10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4C5BAB1DD346C925 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5146
                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1637;
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                                                                                                  Query Match
Best Local S
Matches 27
                                                                                                                                        SMART; SM00216; VWD; 3.

PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.

PROSITE; PS01225; CTGK_2; 1.

PROSITE; PS01285; FA58C_1; 1.

PROSITE; PS01286; FA58C_2; 1.

PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 2.

R PROSITE; PS01209; LDLRA_1; 7.

R PROSITE; PS01209; LDLRA_1; 7.

R PROSITE; PS01209; LDLRA_2; 9.

PROSITE; PS50068; LDLRA_2; 9.

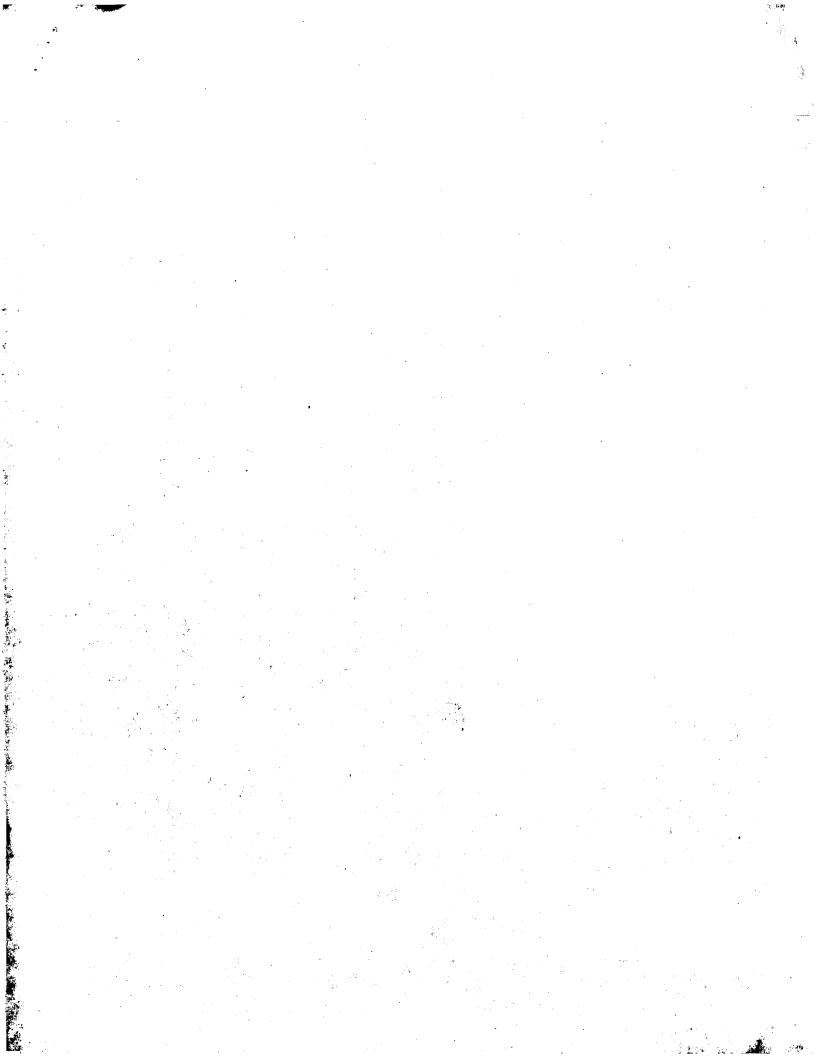
PROSITE; PS50092; TSP1; 25.

R PROSITE; PS50092; TSP1; 25.

R PROSITE; PS01208; VWFC; 1.
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                                                4989 GRPHPPGSEWQK-ACESCRCVSGESIC-TQHCPPLTCAQGETAVQEPGGCCPTCRQEAPE
                        174
                                                             117 GESHANNTKWKKDACTICECKDGQVTCFVEACPPATCA---VPVNIPGACCPVCLQKRAE
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SM00216;
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173 5046

Search completed: July 24, 2003, 12:56:48 Job time: 24.7719 secs



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Result
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PS01186;
PS50092;
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NCBI_TaxID=8355;
                                                                                                                      Developmental
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SEQUENCE
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specific homeobox genes.";
Cell 79:779-790(1994).

-I FUNCTION: POTENT DORSALIZING FACTOR. HAS POTENT AXIS-FORMING
ACTIVITIES INCLUDING THE ABILLTY TO RECRUIT NEIGHBORING CELLS INTO
SECONDARY AXES, REGULATES CELL-CELL INTERACTIONS IN THE ORGANIZING
CENTERS OF HEAD, TRUNK AND TAIL DEVELOPMENT.

-I SUBSCLIDLAR LOCATION: Secreted.
-I- TISSUE SPECIFICITY: PRECORDAL PLATE, NOTOCHORD, CHORDONEURAL
HINGE; EXPRESSION CLOSELY FOLLOWS THE AREAS OF THE EMBRYO THAT
EXPRESS GOOSECOLD AND XNOT2.
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Chordin precursor (Organizer-specific secreted Xenopus laevis (African clawed frog).
                                                                                                                                                   SMART; SM00566; SOG; 3.
SMART; SM00214; VWC; 4.
PROSITE; PS01208; VWFC_1;
PROSITE; PS50184; VWFC_2;
                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-95094250; PubMed-8001117; Sasai Y., Lu B., Steinbeisser H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Amphibia; Batrachia; Anura; Me
                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                        EMBL; L35764; AAC42222.1;
                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                 DEVELOPMENTAL STAGE: EMBRYOGENESIS. SIMILARITY: BELONGS TO THE CHORDIN F SIMILARITY: Contains 4 VWFC domains.
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Anura; Mesobatrachia; Pipoidea; Pipidae;
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RESULT 3
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Best Local S
Matches 43
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MEDLINE=2158823; PubMed=11590138;

Misenheimer T.M., Hahr A.J., Harms A.C., Annis D.S., Mosher D.F.;

"Disulfide connectivity of recombinant C-terminal region of human thrombospondin 2.";

J. Biol. Chem. 276:45882-45887(2001).

-i- FUNCTION: ADHESIVE GLYCOPROTEIN THAT MEDIATES CELL-TO-CELL AND -i- FUNCTION: ANDESIVE GLYCOPROTEIN THAT MEDIATES (BLYCOPROTEIN).
This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no resture by non-profit institutions as long as its content
                                                                                                                                                                                                 -!- SUBUNIT: Homotrimer; disulfide-linked.
-!- SIMILARITY: BELONGS TO THE THROMBOSPONDIN
-!- SIMILARITY: Contains 1 VWFC domain.
-!- SIMILARITY: Contains 3 EGF-like domains.
-!- SIMILARITY: Contains 3 TSP type-1 domains.
-!- SIMILARITY: Contains 7 TSP type-3 domains.
-!- SIMILARITY: Contains 1 TSP N-terminal (TSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Fibropiase,
MEDLINE=92217961; PubMed=1559694;
MEDLINE=92217961; PubMed=1559694;
Labell T.L., McGookey Milewicz D.J., Disteche C.M., Byers P.H.;
Labell T.L., mcGookey Milewicz D.J., Disteche C.M., Byers P.H.;
Labell T.L., mcGookey Milewicz D.J., Disteche C.M., Byers P.H.;
Labell T.L., mcGookey Milewicz D.J., Disteche C.M., Byers P.H.;
Labell T.L., mcGookey Milewicz D.J., Disteche C.M., Byers P.H.;
Labell T.L., mcGookey Milewicz D.J., Disteche C.M., Byers P.H.;
Labell T.L., mcGookey Milewicz D.J., Disteche C.M., Byers P.H.;
Labell T.L., mcGookey Milewicz D.J., Disteche C.M., Byers P.H.;
Labell T.L., mcGookey Milewicz D.J., Disteche C.M., Byers P.H.;
Labell T.L., mcGookey Milewicz D.J., Disteche C.M., Byers P.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Labell T.L., McGookey Milewicz D
"Thrombospondin II: partial cDNA
expression of a second member of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Labell T.L., Byers P.H.; "Sequence and characterization of the complete human thrombospondin 2 CDNA: potential regulatory role for the 3' untranslated region."; Genomics 17:225-229(1993).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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01-JUN-1994
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MEDLINE=94010892; PubMed=8406456;
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28-FEB-2003
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of the thrombospondin gene
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                                          http://www.isb-sib
                                                               Usage
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Pfam; PF02412; tsp_3; 9.
Pfam; PF02210; TsPN; 1.
Pfam; PF00093; vwc; 1.
SMART; SM00218; EGF; 3.
SMART; SM00210; TSPN; 1.
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InterPro; IPR003129;
InterPro; IPR001007;
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PS50092;
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PS01186; EGF_2;
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                                                          TSP TYPE-1 1.
TSP TYPE-1 2.
TSP TYPE-1 3.
EGF-LIKE 1, CALCIUM-BINDING (POTENT EGF-LIKE 3)
EGF-LIKE 3, CALCIUM-BINDING (POTENT EGF-LIKE 3)
TSP TYPE-3 1.
TSP TYPE-3 2.
TSP TYPE-3 5.
TSP TYPE-3 5.
TSP TYPE-3 7.
C-TERMINAL
CELL ATTACHMENT SITE (POTENTIAL).
INTERCHAIN (PROBABLE).
INTERCHAIN (PROBABLE).
BY SIMILARITY.
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TSP N-TERMINAL
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                                                                                                                                                                          Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ADHESIVE GLYCOPROTEIN THAT MEDIATES CELL-TO-CELL CELL-TO-MATRIX INTERACTIONS. CAN BIND TO FIBRINGGEN, FIBRO
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-522 FROM N.A.
MEDLINE=96331130; PubMed=8698834;
Lafeuillade B., Pellerin S., Kera
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Danik M., Chinn A., Lafeuillade M., Keramidas M., Aguesse-Germon Penhoat A., Chen H., Mosher D., Chambaz E.M., Feige J.J.; Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Cetartiod
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THBS2 OR TSP2 OR
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Zafar R.S., Moll Y.D., Womack J.F., Walz D.A.;
"Cloning and sequencing of bovine thrombospondin
TGF-beta.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                   'Opposite regulation of thrombospondin-1
                                            LAMININ AND TYPE V COLLAGEN.
SUBUNIT: HOMOTIMER; disulfide-linked.
SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.
SIMILARITY: Contains 1 VWFC domain.
SIMILARITY: Contains 3 EGF-like domains.
SIMILARITY: Contains 3 TSP type-1 domains.
SIMILARITY: Contains 7 TSP type-3 domains.
SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
    SWISS-PROT entry
een the Swiss Ins
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25; Conserv
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in adrenocortical cells.";
  Physiol. 167:164-172(1996).
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    jht. It is produced through a collaboration
Bioinformatics and the EMBL outstation -
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      InterPro; IPRO01881; EGF_Ca.
InterPro; IPRO06209; EGF_Like.
InterPro; IPRO06210; IEGF_Like.
InterPro; IPRO06210; TSP1.
InterPro; IPRO0367; tsp_3.
InterPro; IPRO03129; TSPN.
InterPro; IPRO03129; TSPN.
InterPro; IPRO03129; TSPN.
InterPro; IPRO03129; Tsp_3.
InterPro; IPRO03129; Tsp_3.
InterPro; IPRO01007; VWF_C.
IPFAm; PF002412; tsp_3.
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IPFAm; PF002412; Tsp_3.
IPFAm; PF002412; Tsp_3.
IPFAm; PF00210; TSPN; 1.
IPFAm; PF000209; TSPN; 3.
IPFAm; SM00210; TSPN; 1.
IPFAM; SM00210; TSPN; 1.
IPROSITE; PS00022; EGF_1; FALSE_N PROSITE; PS001206; TSP1; 3.
IPROSITE; PS001206; VWFC_1; 1.
IPROSITE; PS001206; VWFC_1; 1.
IPROSITE; PS001206; VWFC_1; 1.
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HSSP; P00740;
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   FALSE_NEG
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TSP TYPE-1 2.
TSP TYPE-1 3.
EGF-LIKE 1.
EGF-LIKE 2, CALCIUM-BINDING (POTENT EGF-LIKE 3.
TSP TYPE-3 1.
TSP TYPE-3 2.
TSP TYPE-3 3.
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TSP TYPE-3 5.
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RESULT 4
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MEDLINE-92147683; PubMed-1371115;

Laherty C.D., O'Rourke K., Wolf F.W.,

Dixit V.M.;
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Q03350;

Q1-JUN-1994 (Rel. 29, Creat

Q1-JUN-1994 (Rel. 29, Last

28-FEB-2003 (Rel. 41, Last
        the
use
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Dixit V.M.;
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-873 FROM N.A.
MEDLINE-91302287; PubMed-1712771;
Bornstein P., O'Rourke K., Wikstrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Characterization of mouse thrombospondin during cell growth and development.";
J. Biol. Chem. 267:3274-3281(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thrombospondin
                                                    between
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                                                                                       LAMININ AND TYPE V COLLAGEN.

SUBUNIT: Homotrimer; disulfide-linked.

SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.

SIMILARITY: Contains 1 TWFC domain.

SIMILARITY: Contains 3 EGF-like domains.

SIMILARITY: Contains 3 TSP type-1 domains.

SIMILARITY: Contains 7 TSP type-3 domains.

SIMILARITY: Contains 7 TSP vpe-3 domains.
                                                                                                                                                                                                                                                                                                                                                              second, expressed thrombospondin gene
                            s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                         Biol. Chem. 266:12821-12824(1991).

FUNCTION: ADHESIVE GLYCOPROTEIN THAT MEDIATES CELL-TO-CELL AND CELL-TO-MATRIX INTERACTIONS. CAN BIND TO FIBRINGEN, FIBRONECTIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117
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MGD; MGI:98738 Thbs2.

InterPro; IPR006209; EGF_1a

InterPro; IPR006210; IEGF

InterPro; IPR000884; TSP1.

InterPro; IPR003129; TSP1.

InterPro; IPR003129; TSP1.

InterPro; IPR003129; TSP1.

InterPro; IPR001007; VWF_C.

Pfam; PF00090; EGF; 2.

Pfam; PF00412; tsp_3; 9.

Pfam; PF00412; tsp_3; 9.

Pfam; PF00412; tsp_1; 3.

Pfam; PF00412; TSPN; 1.

Pfam; PF00412; TSPN; 1.

SMART; SW0018; EGF; 3.

SMART; SW0010; TSP1; 3.

SMART; SW00210; TSP1; 3.

PROSITE; PS01106; EGF_1; FA

PROSITE; PS01106; WFC_1; 1.

PROSITE; PS01108; VWFC_1; 1.

PROSITE; PS01108; VWFC_1; 1.
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"Nel homolog gene expression in craniofacial anomalies.";
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=97131504; PubMed=8975702;
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SUBUNIT: HOMOTRIMER. BINDS TO PKC BETA-1 (BY SIMILARITY).
SUBCELLULAR LOCATION: Secreted (By similarity).
DISEASE: EXPRESSED IN CRANIOFACIAL ANOMALIES.
SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
SIMILARITY: Contains 5 VWFC domains.
SIMILARITY: Contains 5 VWFC domains.
SIMILARITY: Contains 6 EGF-like domains.
CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAIL POSITIONS 427 AND 771.
                                                              European Bioinformatics Institute.
                                                                                    SWISS-PROT entry is copyright. It is produced en the Swiss Institute of Bioinformatics and
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        and
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                                   way
          Pfam; PF02210; TSPN; 1.
Pfam; PF00293; VWC; 2.
SMART; SM00179; EGF_CA; 2.
SMART; SM00210; TSPN; 1.
SMART; SM00210; TSPN; 1.
SMART; SM00214; VWC; 3.
SMART; SM00214; VWC; 3.
PROSITE; PS00010; ASX_HUDF
PROSITE; PS00022; EGF_1; 1
PROSITE; PS01186; EGF_2; 3
PROSITE; PS01187; EGF_CA; PROSITE; PS01108; VWFC_1; PS01208; VWFC_1; PROSITE; PS01208; VWFC_2; PROSITE; PS01208; PVFC_2; PROSITE; PS01208; PVFC_2; PROSITE; PS01208; PVFC_2; PROSITE; PS01208; PVFC_2; PVFC
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EMBL; U57523; AABO69
HSSP; P07204; 1ADX.
Genew; HGNC:7750; NI
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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2; PS00022; EGF 1; 1.

3; PS01186; EGF 2; 3.

3; PS01187; EGF CA; 3.

3; PS01208; VWFC_1; 2.

5; PS50184; VWFC_2; 2.
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        domain;
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WHEC 2.

EGF-LIKE 1.

EGF-LIKE 3.

EGF-LIKE 3.

EGF-LIKE 5, CALCII

EGF-LIKE 5, CALCII

EGF-LIKE 6, CALCII

EGF-LIKE 6, CALCII

EGF-LIKE 5.

EGF-LIKE 10, CALCII

EGF-LIKE 5, CALCII

EGF-LIKE 5, CALCII

EGF-LIKE 6, CALCII

VWFC 10

EY SIMILARITY

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PROTEIN KINASE OF N-TERMINAL.
WHEC 1.
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     (POTENTIAL).
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Best Local S
Matches 32
Pfam; PF00093; vwc; 2.
SMART; SM00179; EGF_CA; 2.
SMART; SM00210; TSPN; 1.
SMART; SM00210; TSPN; 1.
SMART; SM00214; VWC; 2.
PROSITE; PS00010; ASX_HYDR
PROSITE; PS00010; EGF_1; 1
PROSITE; PS01186; EGF_2; 3
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CONFLICT
SEQUENCE
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Eukaryota; Metazoa; Chorv
Mammalia; Eutheria; Roder
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
Protein kinase C-binding protein NELL1 prec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEL1_RAT
Q62919;
                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Blochemical characterization and expression analysis thrombospondin-1-like proteins NELL1 and NELL2."; Biochem. Biophys. Res. Commun. 265:79-86(1999).
-!- SUBUNIT: HOMOTRIMER. BINDS TO PKC BETA-1.
                                                                                                                                                                                                                                                                        EMBL; U48246; AAC72252.1;
PIR; T10756; T10756.
HSSP; P35555; 1EMN.
                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as i modified and this statement is not removed. Us
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- SUBCELLULAR LOCATION: Secreted.
-i- SIMILARITY: Contains 1 TSP N-terminal (TSPN)
-i- SIMILARITY: Contains 5 WFC domains.
-i- SIMILARITY: Contains 6 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Sprague-Dawley; MEDLINE=20017976; PubMe
                                                                                                                                         Pfam;
                                                                                                                                                                                                                                                                                                                                                           entities requires
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kuroda S., Oyasu M., Kawakami M., Kanayama N., Tanizawa K., Saito
Abe T., Matsuhashi S., Ting K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                         InterPro;
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32; Conser
                                                                                                                                                  3; IPR000152; Asx_hydroxyl.
3; IPR001881; EGF_Ca.
3; IPR001801; EGF_like.
5; IPR001791; Laminin_G.
5; IPR003129; TSPN.
5; IPR001007; VWF_C.
600008; EGF; 5.
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                                                                                                                                      TSPN;
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 ; ASX_HYDROXYL;
; EGF_1; 1.
; EGF_2; 3.
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Rodentia;
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C -> H (IN REF. 2).
S -> C (IN REF. 2).
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 Homo sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria; 
                                                   NRLN1.
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RESULT 8
NRL1_HUMAN
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Best Local S
Matches 31
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DOMAIN
DISULFID
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CARBOHYD
CARBOHYD
               NRL1_HUMAN STANDARD; PRT; 09BU40; Q9Y3H7; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence up 15-SEP-2003 (Rel. 42, Last annotation
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SEQUENCE
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Neuralin
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                                                                                                                                                                  298
                                                                                                                                                                                                                                                               78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS01187; EGF_CA;
PS01208; VWFC_1;
PS50184; VWFC_2;
                                                                                                                                                                               KDGQVTCFVEACPPATC---AVPVNIPGACCPVCLQK
                                                                                                                                                                  KSGAVECRRMSCPPLNCSPDSLPVHISGQCCKVCRPK 334
                                                                                                                                                                                                                               GIMDLQELLAKMTAKLNYAETRLGQLENCHCEKTC-QVSGLLYRDQDSWVDGDNCGNCTC
                                                                                                                                                                                                                                                             GTNDFREFVLEMQKTITDLRTQIKKLESRLSTTECVDAGGESHANNTKW-KKDACTICEC
                                                                                                                                                                                                                                                                                                                                                            418
448
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 (Ventroptin)
                                                                                                                                                                                                                                                                                                              14.0%;
32.0%;
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                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY
BY
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EGF-LIKE 2. CALCIUM-BINDING ()
EGF-LIKE 4.
EGF-LIKE 5. CALCIUM-BINDING ()
EGF-LIKE 6. CALCIUM-BINDING ()
WHEC 3.
VMFC 4.
VMFC 5.
                                                                                                                                                                                                                                                                                           Score 134.5;
Pred. No. 0.00
L4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILA
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PROTEIN KINASE C
PROTEIN KINASE C
TSP N-TERMINAL.
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                update)
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                                                                                                                                                                                                                                                                                             47;
                                                                                                                                                                                                                                                                                                                           1.
                                                                                                                                                                                                                                                                                                                                                               CRC64;
                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                             810;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                             5.
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                               297
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Chordata; Primates;

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

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                                                          RESULT 9
                      NRL1_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Ra Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Ra Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Ra Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Ra Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Ra Altschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.E., Schaelton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Ra Stapleton M.J., Gulin T.B., Toshiyuki S., Carninci P., Prange C., Ra Rownstein M.J., Udin T.B., Toshiyuki S., Carninci P., Prange C., Ra Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H., Ra Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Ra Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Ra Fahey J., Helton E., Ketteman M., Maddan A., Rodrigues S., Sanchez A., Ra Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Ra Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Ra Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Ra Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Ra Rodriguez A.C., Grimwood J., Schmutz J.M., Marra M.A.; Thench M.S., Jones S.J.M., Marra M.A.; Thench M.S., Jones S.J.M., Marra M.A.; Thench M.S., Schein J.E., Jones S.J.M., Marra M.A.; Thench M.S., Schein J.S., Jones S.J.M., Marra M.S., Schein J.S., Jones S.J.
                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use as long as its content use as long as long as its content use as long as long
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-- FUNCTION: Seems to antagonize the function of BMP-4 by binding to the state of the function of the similarity).

-- SUBCELLULAR LOCATION: Secreted (Potential).
NRL1_CHICK
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS01208; VWFC_1; 3. PROSITE; PS50184; VWFC_2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001007; VWF_C.
Pfam; PF00093; vwc; 3.
SMART; SM00214; VWC; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; BC002909; AAH02909.1; EMBL; AL049176; CAB42789.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pearce A
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[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           it and preventing its iteraction wit
SUBCELLULAR LOCATION: Secreted (Pote
SIMILARITY: Contains 3 VMFC domains.
                                                                                                                                   136
                                                                                                                                                                 131 CTICECKDGQVTCFVEACPPATCAVPVNIPGACCPVC 167
                                                                                                                                                                                                                                          l Similarity
19; Conser
                                                                                                                                CTQCSCSEGNVYCGLKTCPKLTCAFPVSVPDSCCRVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS01208;
                                                                                                                                                                                                                                                                                                                                                 323
450 AA;
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107
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173
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285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein;
     STANDARD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sci.
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450
94
173
317
175
112
285
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                                                                                                                                                                                                                                                                13.4%;
51.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat;
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                                                                                                                                                                                                                                                                                                                                                    MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VWFC
VWFC
                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
E -> EE (IN REF. 2).
                                                                                                                                                                                                                                                                      Pred.
                                                                                                                                                                                                                                                                                            Score 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEURALIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99:16899-16903(2002).
     PRT;
                                                                                                                                                                                                                                                                                                                                                    D5F39AB9E2EE3E71 CRC64;
                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTACHMENT SITE (POTENTIAL).
                                                                                                                                                                                                                                                                      No.
  456
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     A
                                                                                                                                                                                                                                                                      . 0006 ;
                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                         Length 450;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ior
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                                                                                                                                                                                                                                    Gaps
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     RR RN OCC OCC DE DE
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RESULT 10
ECM2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                          Matches
                                                                                                    28-FEB-2003 (Rel. 4
28-FEB-2003 (Rel. 4
28-FEB-2003 (Rel. 4
28-FEB-2003 (Rel. 4
Extracellular matri
SC1/ECM2).
                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0902D5;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Reuralin precursor (Ventroptin).
NRLNI OR VOPT.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                      SITE
                         Mammaila; Eutheria; Primates; NCBI_TaxID=9606; . [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use
                                                                                                                                                                       ECM2_HUMAN 094769;
                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a obetween the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pattern in the retina.";
Science 293:111-115(2001).
-!- FUNCTION: Seems to antagonize the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sakuta H., Suzuki R., Takahashi H., Kato A., Iemura S.-I., Yamamoto T.S., Ueno N., Noda M "Ventroptin: a BMP-4 antagonist expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS01208; VWFC_1; 3: PROSITE; PS50184; VWFC_2; 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00214; VWC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001007; V
Pfam; PF00093; vwc; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF257352; AAK73359.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21334726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archosauria; Aves;
SEQUENCE FROM N.A.
MEDLINE=99009324;
                                                                            Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                         Local Similarity hes 18; Conser
                                                                                                                                                                                                                                                      144 CAQCSCSEGNVYCGLKTCPKLTCSFPVSVPESCCPVC
                                                                                                                                                                                                                                                                             131 CTICECKDGQVTCFVEACPPATCAVPVNIPGACCPVC 167
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                                                                                                                                                                                                                                                                                                                                                       295
456
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181
120
                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                   matrix
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                                                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                    28
456
183
120
295
52399.

    Last sequence update)
    Last annotation update)

                                                                                                                                            41, Created)
41, Last seg
 PubMed=9790758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=11441185;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION,
                                                                                                                                                                                                                                                                                                                     13.4%;
                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Repeat;
                                                                                                                                                                                                                                                                                                                                                              MW;
                                                                                                                                                                                                                                                                                                                     Score 129; F
                                                                                                                   N
                                                                                                                                                                                                                                                                                                         Pred. No. 0.0
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                  CELL ATTACHMENT SITE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                   NEURALIN.
                                                                                                                                                                                                                                                                                                                                                                                                                             ; Glycoprotein; Signal POTENTIAL.
                                                  Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                   precursor (Matrix glycoprotein
                                                                                                                                                                                                                                                                                                                                                              D54F6685F3839BC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             function of BMP-4 by binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       There are no restrictions
                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                     AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND FUNCTION
                                                   Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ventral retina.
                                                                                                                                                                                                                                                                                                                                Length 456;
                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
                                                                 Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a collaboration
                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     outstation
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                                                                                           Query Match
Best Local :
                                                                                  Matches
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InterPro; IPR003591; LRR_LYP.
InterPro; IPR001007; VWF_C.
Pfam; PF00560; IRP. 1^
                                                                                                                        CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                          DOMAIN
REPEAT
REPEAT
                                                                                                                                                                          REPEAT
REPEAT
DOMAIN
                                                                                                                                                                                                                                                                                                                                     Signal.
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                                                                                                                                                                  SITE
                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                             REPEAT
REPEAT
                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS01208; VWFC_1; PROSITE; PS50184; VWFC_2;
                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00019; LEURICHRPT SMART; SM00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00560; LRR; Pfam; PF00093; vwc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            uterus.
-!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             female-specific tissues and its chromosomal localization to 9q22.3.", Genomics 52:378-381(1998).
i- SUBCELIUIAR LOCATION: Secreted; extracellular matrix.
i- TISSUE SPECIFICITY: Expressed predominantly in adipose tissue as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Identification of a novel gene (ECM2) encoding a putative extracellular matrix protein expressed predominantly in adipose and
                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB011792; BAA33958.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nishiu
                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                                                                       Leucine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SLRPS) FAMILY.
SIMILARITY: Contains 1 VWFC domain.
SIMILARITY: Contains 12 leucine-rich (LRR) repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO:0005578; C:extracellular matrix;
GO:0005578; F:integrin binding activ
GO:0005176; P:cell-matrix adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    well as female-specific organs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           603479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J.,
                                        18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HGNC:3154; ECM2.
                                                                                  40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 an email to license@isb-sib.ch).
                                                                                         Similarity
                   NDFREFVLEMQKTITDLRTQIKKLESRLSTTECVDAGGESHA-----NNTKWKKDAC
                                         DFGKNEEIPRKQRRKIYHRRLRKSSTSHKHRSNRQLGIQQTTVFTPVARLPIVNFDYSME
                                                           EFSYQEDKPTKKTRP---RKIPSVGRQGEHLSN----STSAFS----TRSDASGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tanaka T.,
                                                                                                                                                                                                        101
101
335
356
382
406
427
427
451
596
                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                       repeat; Repeat;
                                                                                                                          A
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699
158
355
426
426
426
447
6497
643
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643
                                                                                            13.2%;
                                                                                                                          79789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nakamura Y.;
                                                                                           . 68;
                                                                                                                          MW.
                                                                                 14;
SSFPGVESSYN----VLPGKKGHCLVKGITMYNKAVWSPEPC
                                                                                                                       CELL ATTACHMENT SITE (POTE)
N-LINKED (GLCNAC. . .) (PO)
                                                                                         Score 127; I
                                                                                Pred. No. 0.00
4; Mismatches
                                                                                                                                                                          LRR-T 7.
LRR-T 8.
POLY-GLU.
                                                                                                                                                                                                                                                           LRR-S
LRR-T
                                                                                                                                                                                                                                                                                                                                                     Glycoprotein;
                                                                                                                                                                                                                             LRR-S
LRR-T
                                                                                                                                                                                                                                                                                                              VWEC.
                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR MATRIX PROTEIN
                                                                                                                                                                ATTACHMENT SITE (POTENTIAL)
                                                                                                                                                                                       trix; TAS.
activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          moved. Usage by and for commercial (See http://www.isb-s1b.ch/announce,
                                                                           D<sub>b</sub>
J.0014;
62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        There are no restrictions
                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                       Extracellular matrix;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mammary gland, ovary, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAS.
                                                                                                   Length 699;
                                                                                Indels
                                                                                                                                  (POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in
                                                                                Gaps
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RESULT ON A COCO OF THE COCO O
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28-FEB-2003 (Rel
28-FEB-2003 (Rel
28-FEB-2003 (Rel
                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sakuta H., Suzuki k., I
Iemura S.-I., Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM BETA).
MEDLINE=20568969; PubMed=11118896;
Coffinier C.C., Tran U., Larrain J., De Robertis
"Neuralin-1 is a novel chordin-related molecule
neural plate.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21334726; PubMed=11441185;
Sakuta H., Suzuki R., Takahashi H., Kato A.,
Iemura S.-I., Yamamoto T.S., Ueno N., Noda M
                                                                                                                                                                                    MGD; MGI:1933172; Nrln1.
InterPro; IPR001007; VWF_C.
Pfam; PF00093; vwc; 3.
SMART; SM00214; VWC; 3.
                                                                                                                                                                                                                                                                                                                  EMBL; AF321853; EMBL; AF296451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mech.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neural plate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pattern in the retina.";
Science 293:111-115(2001).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NRLN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neuralin precursor (Ventroptin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NRL1_MOUSE
                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Ventroptin: a BMP-4 antagonist expressed in pattern in the retina.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                      Alternative
                                                                                                           Developmental protein;
                                                                                                                                     PROSITE; PS01208; VWFC_1; PROSITE; PS50184; VWFC_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEVELOPMENTAL STAGE: Expression starts in the neural plate a gastrulation. Later on its expression becomes restricted to discrete regions of the central nervous system and to derivate neural crest cells.

SIMILARITY: Contains 3 VWFC domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: Seems to antagonize the function of BMP-4 it and preventing its iteraction with receptors (By SUBCELLULAR LOCATION: Secreted (Potential) ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=2;
Name=Alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=Beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and testis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 TICECKDGQVTCFVEACPPATCAVPVNIPGACCPVC
                                                                                                                                                                                                                                                                                          AF305714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q920C1-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=Q920C1-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTCLCSDGRVLCDETMCHPQRCPQTVIPEGECCPVC
Al prote

Al prote

/e splicing.

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95
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(Rel. 41, Last sequence up)
(Rel. 41, Last annotation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                          AAG27460.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9EPZ9;
                                                                                                                                                                                                                                                                                                               AAK95586.1;
AAK71523.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence=VSP_001076, VSP_001077;
Y: Expressed in heart, brain, lung,
                                                                                                                Repeat;
                                                                                                                                                                                                                                                                                          . . .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                           Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               De Robertis E.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shintani T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          he EMBL outstation restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            by binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                liver,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               derivatives
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a collaboration -
MBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           at mid-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                kidney
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SIGNAL CHAIN

NEURALIN.

POTENTIAL

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TSP1_HUMAN
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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CARBOHYD
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P07996; Q15667;
01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
DOMAIN
                                                                                                                                                                    "Partial amino acid sequence of human analysis of cDNA clones: homology to m proteins.";
                                                                                                                                                                                                                                                     "Complete thrombospondin mRNA sequence includes potential regulatory sites in the 3' untranslated region.";
J. Cell Biol. 108:729-736(1989).
                                                                                                                                                                                                                                                                                                                                                                                  TEQUENCE FROM N.A.
TISSUE-Endothelial cells;
MEDLINE-87057617; PubMed=2430973;
Lawler J., Hynes R.O.;
"The structure of human thrombospondin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thrombospondin 1 precursor. THBS1 OR TSP1 OR TSP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SITE
                                                                                          MEDLINE=86287276; PubMed=3461443;
Dixit V.M., Hennessy S.W., Grant G.A.
"Characterization of a cDNA encoding
                                                                                                                                                                                                                                                                                                                                                                 multiple calcium-binding
proteins.";
Laherty C.D., Gierman T.M., Dixit V.M.; "Characterization of the promoter region of gene. DNA sequences within the first intron
                                                                                    domains of
                                                                                                                                                                                                                                                                                         Hennessy S.W., Frazier B.A., Kim D.D., Baumgartel D.M., Rotwein P., Frazier W.
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE-89139590; PubMed-2918029;
                                                                                                                                                                                                                  SEQUENCE OF 1-397 FROM N.A. MEDLINE=87157592; PubMed=3030396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                  SEQUENCE OF 1-166 FROM N.A. MEDLINE=89291870; PubMed=2544587;
                                                                                                                                   SEQUENCE OF
                                                                                                                                                         Biochemistry 25:8418-8425(1986).
                                                                                                                                                                                                                                                                                                                                                   Cell Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN
                                                                         Natl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTICECKDGQVTCFVEACPPATCAVPVNIPGACCPVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CSQCSCSEGNVYCGLKTCPKLTCAFPVSVPDSCCRVC 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 211
447
                                                                                    human
                                                                                                                                  1-374 FROM N.A.
                                                                         Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .334
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253
174
113
286
319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΑĄ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                      thrombospondin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50732 MW;
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                                                                                                                                                                                                                                                                                                                                                                         sites and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Missing (in isoform /FTId=VSP_001077.
N -> S (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VWFC 2.

VWFC 3.

CELL ATTACHMENT SITE (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

EEPPSQNFDSKGSFC -> GKKAKGALAGGPAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTId=VSP_001076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isoform Beta)
                                                                        83:5449-5453(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -> S (IN REF. 2).
94C999025A97545D CRC64;
                                                                                       c'G.A., ng the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                        Framson P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125; DB 1;
No. 0.0013;
                                                                                                                                                                                                                                                                                                                                                                       ndin, an adhesive glycoprotein with homologies with several different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1170 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
                                                                                                                                                                                n thrombospondin as determined
malarial circumsporozoite
                                                                                                         Rotwein P.,
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            the human thrombospondin
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                                                                                                                                                                                                       Bornstein P.;
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                                                                                              ., Frazier W.A.;
and collagen bi
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Pfam; F Pfam; F Pfam; F Pfam; F Pfam; F SMART;

PF02210; PF02412;

PF00008; EGF; 2.
PF00099; tsp_1; 3.
PF00099; twc; 1.
PF02210; TSPN; 1.
PF02412; tsp_3; 8.
PF02412; tsp_3; 8.
PF02412; tsp_3; 8.
PF02412; tsp_3; 8.
PF02412; tsp_1; 3.

InterPro; InterPro;

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EMBL; M25631; AAA36741.1; EMBL; X04665; CAA28370.1; -EMBL; X14787; CAA32889.1; -EMBL; M14326; AAA61237.1; AEMBL; J04835; AAA61178.1; -EMBL; M994255; AAB59366.1; -EMBL; M994255; AAB59366.1; -
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[6]
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"Biophysical characterization, including disulfide bond assignments, of the anti-angiogenic type 1 domains of human thrombospondin-1.";
Biochemistry 41:14329-14339(2002)
-!- FUNCTION: Adhesive glycoproteain that mediates cell-to-cell and cell-to-matrix interactions. Can bind to fibrinogen, fibronectin, laminin, type V collagen and integrins alpha-V/beta-1, alpha-
                                                                                                                                                                                      InterPro;
InterPro;
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GlycoSuiteDB; P07996; -
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Mosher D.F., Peter-Katalinic
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                                                                                                                     ; IPR001881; EGF_Ca.; IPR006209; EGF_like.; IPR006210; IEGF.; IPR006811; IEGF.; IPR003367; tsp_3.; IPR003367; tsp_3.; IPR003129; TSPN.; IPR003129; TSPN.; IPR001007; VWF_C.
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(XXX-1992) to the EMBL/GenBank/DDBJ
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184; VWFC_2; 1.
Cell adhesion; Calcium-Lin; Signal; 3D-structure
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TSP TYPE-1 1.

TSP TYPE-1 3.

EGF-LIKE 1.

EGF-LIKE 2. CALCIUM-BINDING (POTENT FOR TYPE-3 1.)

TSP TYPE-3 2.

TSP TYPE-3 3.

TSP TYPE-3 4.

TSP TYPE-3 5.

TSP TYPE-3 7.

CTERMINAL.

CLL ATTACHMENT SITE (POTENTIAL).

INTERCHAIN (PROBABLE).

INTERCHAIN (PROBABLE).
/FTId-CAR_000210.
O-LINKED (FUC. .)
/FTId-CAR_000211.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                                                                                        /FTId=CAR_000205.
O-LINKED (FUC. . . . /FTId=CAR_000206.
C-LINKED (MAN).
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HEPARIN-BINDING
TSP N-TERMINAL.
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/FTId=CAR_000209.
C-LINKED (MAN).
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C-LINKED (MAN).
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TSP1_MOUSE
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01-JUN-1994
01-JUN-1994
28-FEB-2003
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CONFLICT
SEQUENCE
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  EMBL; M62470; AAA50611.1;
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                   an
                   email to license@isb-sib.ch).
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cell-to-matrix interactions. Can bind to fibrinogen, tib;
laminin, type V collagen and integrins alpha-V/beta-1, a.
V/beta-3 and alpha-IIb/beta-3.

-!- SUBUNIT: Homotrimer; disulfide-linked.

-!- SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.

-!- SIMILARITY: Contains 1 VWFC domains.

-!- SIMILARITY: Contains 3 TSP type-1 domains.

-!- SIMILARITY: Contains 7 TSP type-3 domains.

-!- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
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                                                                                                                                                                                                                                                                                                                     Bornstein P., Alfi D., Devarayalu S., Framson P., Li P.;
"Characterization of the mouse thrombospondin gene and evaluation
the role of the first intron in human gene expression.";
J. Biol. Chem. 265:16691-16698(1990).
-!- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and
cell-to-matrix interactions. Can bind to fibrinogen, fibronect
laminin, type V collagen and integrins alpha-V/beta-1, alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=92147683; PubMed=1371115;
Laherty C.D., O'Rourke K., Wolf F.W.,
Dixit V.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          during cell growth and development.
J. Biol. Chem. 267:3274-3281(1992).
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"Characterization of the
Genomics 11:587-600(1991)
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THBS1 OR TSP1.
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te M., Ferro P.,
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3; Mismatches 47;
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Sciurognathi; Muridae;
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> A (IN REF. 2).
69B3EDE5AE3A395E CRC64;
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; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                              fibronectin,
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InterPro; IPR003129; TSPN
InterPro; IPR001007; VWF_C
Pfam; PF00008; EGF; 2;
Pfam; PF00009; tsp_1; 3;
Pfam; PF02210; TSPN; 1;
Pfam; PF02210; TSPN; 1;
SMART; SM00210; TSPN; 1;
SMART; SM00210; TSPN; 1;
SMART; SM00214; VWG; 1;
SMART; SM00214; VWG; 1;
SMART; SM00214; VWG; 1;
SMART; SM00214; VWG; 1;
PR0SITE; PS00128; EGF_2; 1;
PROSITE; PS00128; EGF_2; 1;
PROSITE; PS01186; EGF_2; 1;
PROSITE; PS01208; VWFC_1;
PROSITE; PS01208; VWFC_1;
PROSITE; PS01208; VWFC_1;
PROSITE; PS01208; VWFC_1;
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InterPro; IPR006209; EGF_1ike.
InterPro; IPR006210; IEGF.
InterPro; IPR00084; TSP1.
InterPro; IPR003367; tsp_3.
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Matches 25
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Eukaryota; Metazoa; C
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NCBI_TaxID=9606;
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16-OCT-2001 (Rel
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CONFLICT
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                                                              SEQUENCE OF 115-955 FROM N.A. (ISC
MEDLINE-99000848; PubMed-9782094;
Pappano W.N., Scott I.C., Clark T.
Greenspan D.S.;
"Coding sequence and expression patterns of mouse chordin and mapping of the cognate mouse chrd and human CHRD genes."; Genomics 52:236-239(1998).
                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).

MEDLLINE=21366001; PubMed=11472837;

MILLET C., Lemaire P., Orsetti B., Guglielmi P., France

"The human chordin gene encodes several differentially

spliced variants with distinct BMP opposing activities.

Mech. Dev. 106:85-96(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                              CHRD.
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Primates;
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Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167
                                                                                       Eddy
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                                                                                          R.L.,
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De Robertis E.M.;

"Bmp binding modules in the chordin patterning protein.";

Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Dorsalizing factor. Key developmental prote
                                                                                                                                                                                                                                                          MIM;
                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/ɛnnounce/or send an email to license@isb-sib.ch).
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SEQUENCE
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                               VARSPLIC
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                                                                                                                        DOMAIN
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                                                                                                                                                                                                                            InterPro; IPR001007; VWF_C. Pfam; PF00093; vwc; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE SPECIFICITY: Expressed at the highe SIMILARITY: BELONGS TO THE CHORDIN FAMILY. SIMILARITY: Contains 4 VWFC domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dorsalizes early vertebrate embryonic tissues by binding to ventralizing TGF-beta family bone morphogenetic proteins () and sequestering them in latent complexes (By similarity). SUBCELLULAR LOCATION: Secreted (By similarity). ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                              Event-Alternative splicing; Named isoforms=5; Comment-Experimental confirmation may be lacking
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15-SEP-2003
SEQUENCE OF 1-463 FROM N.A.

MEDLINB-89123368; PubMed-2914927;

Woodbury D., Benson-Chanda V., Ramirez F.;

Woodbury D., Benson-chanda V., Ramirez F.;

"Amino-terminal propeptide of human pro-alpha 2(V) collagen conforms to the structural criteria of a fibrillar procollagen molecule.";

J. Biol. Chem. 264:2735-2738(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                               Tsipouras
Ramirez F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDITIE=87146331; PubMed=3029669; Medi D., Bernard M.P., Gargano S., Ra "The pro alpha 2(V) collagen gene is major fibrillar forming collagens.";
                                                                                                                                                                                                                                                                                                                                        MEDLINE=85289337; PubMed=2411731; Myers J.C., Loidl H.R., Seyer J.M., "Complete primary structure of the COOH-terminal propeptide.";
                                                                                                                                                                                                                                                                   SEQUENCE OF 1449-1496 FROM MEDLINE=89138450; PubMed=32
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1227-1496 FROM N.A. MEDLINE-85289337; PubMed=2411731;
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Mammalia; Eutheria;
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                                                                                              TISSUE=Placenta;
MEDLINE=92239022;
                                                                                                                                  SEQUENCE OF
                                                                                                                                                                      "Genetic distance of two filocated on the long arm of Genomics 3:275-277(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic
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                                                                                                                                                                                                                                               P., Schwartz R.C., Liddell A.C.,
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RQLP -> QVAA (IN REF. 2).
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InterPro; IPR000087; Collagen.
InterPro; IPR000885; Fib_collagen_C.
InterPro; IPR001007; VWF_C.
Pfam; PF01410; COLFI; 1.
Pfam; PF01391; Collagen; 18.
Pfam; PF00393; vwc; 1.
ProDom; PD000007; Clg_helix; 5.
ProDom; PD002078; Fib_collagen_C; 1.
SMART; SM00038; COLFI; 1.
                                                                                                                                                                                                                                                                                           EMBL; J04478; AAA51859.1; -.
EMBL; X04758; CAA28454.1; -.
EMBL; M11718; AAA52058.1; -.
PIR; A31427; CGHU2V.
PDB; 1A9A; 18.NOV-98.
Genew; HGNC:2210; COL5A2.
MIM; 120190; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Med. Genet. 35:846-848(1998).

J. Med. Genet. 35:846-848(1998).

FUNCTION: TYPE V COLLAGEN IS A MEMBER OF GROUP I COLLAGEN
(FIBRILLAR FORMING COLLAGEN). IT IS A MINOR CONNECTIVE TISSUE
COMPONENT OR NEARLY UBFOUTOUS DISTRIBUTION. TYPE V COLLAGEN BINDS
TO DNA, HEPARAN SULFATE, THROMBOSPONDIN, HEPARIN, AND INSULIN.

SUBUNIT: TRIMERS OF TWO ALPHA 1(V) AND ONE ALPHA 2(V) CHAINS IN
MOST TISSUES AND TRIMERS OF ONE ALPHA 1(V), ONE ALPHA 2(V), AND
ONE ALPHA 3(V) CHAINS IN PLACENTA.

PTM: PROlines at the third position of the tripeptide repeating
unit (G-X-Y) are hydroxylated in some or all of the chains.

LOUSAS are a cause of Ehlers-Danlos syndrome
type I (EDS-I) [MIM:130000]; also known as Ehlers-Danlos syndrome
type I (EDS-I) is an autosomal dominant connective-tissue disorder
characterized by loose-jointedness and fragile, velvety,
stretchable, bruisable skin that heals with peculiar 'cigarette-
paper' scars. Inheritance is autosomal dominant.

-! DISEASE: Defects in COLSA2 are a cause of Ehlers-Danlos syndrome
type II (EDS-II) [MIM:130010]; also known as Ehlers-Danlos syndrome
syndrome mitis. Inheritance is autosomal dominant.

-! SIMILARITY: Contains 1 VWFC domain.
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II.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-98087576; PubMed-9425231; Milling M.C., Wenstrup R.J., Cole W.G.; Michalickova K., Susic M., Willing M.C., Wenstrup R.J., Cole W.G.; "Mutations of the alpha2(V) chain of type V collagen impair matrix assembly and produce Ehlers-Danlos syndrome type I."; Hum. Mol. Genet. 7:249-255(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eur. J. Biochem. 221:987-995(1994).
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MEDLINE=94237164;
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                                                                                                                                                                                                GO:0005588; C:collagen type V; TAS.
GO:0005202; F:collagen; TAS.
GO:0008151; P:cell growth and/or maintenance; TAS
         SM00038; COLFI;
SM00214; VWC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Martin S., Nicholls A.C., Harrison J.B., Pope F.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Rousseau J.C., Kleman J.P., Champliaud M.F., Bernillon J., Wallach J.M., van der Rest M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (See http://www.isb-sib.ch/announce/
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PROSITE; PS50184; VWFC_2; 1.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Glycoprotein; Collagen; Signal; Ehlers-Danlos syndrome;
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                                                                                                                                                                                                                           Disease mutation;
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                                                                                                                                                            MOD_RES
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                117 GESHANNTKWKKDACTICECKDGQVTC-FVEACPPATCAVPVNIPGACCPVCLQ 169
$
                                          Similarity
GQMYLNRDIWKPAPCQICVCDNGAILCDKIECQDVLDCADPVTPPGECCPVCSQ
                                                                    292
1418
1438
1460
1496
1496
                                  Conservative
                                                                                                                                 290
293
296
608
614
960
                                                                    AA;
                                                                            1460
                                                                                                       292
1418
                                                                                                                                 1226
1496
97
290
293
296
608
614
                                         12.8%;
                                                                                                                                                                                                                           structure.
                                                                    144720
                                                                          HYDROXYLATION.

GENERAL OLDER (IN EDS-II).

/FTId VAR_O13588.

A -> P (IN REF. 6).

K -> T (IN REF. 3).

F -> S (IN REF. 4).

V -> A (IN REF. 4).
                                  5.
                                                                     ₹,
                                Score 123.5; DB Pred. No. 0.0065; 5; Mismatches 2
                                                                                                                                                                                               COLLAGEN ALPHA 2(V) CHAIN CARBOXYL-TERMINAL PROPERT
                                                                                                                                                    HYDROXYLATION
                                                                                                                                                             HYDROXYLATION
                                                                                                                                                                     HYDROXYLATION
                                                                     82827C17A8644F5A CRC64;
                                  25;
                                                  ۲,
                                                 Length 1496;
                                  Indels
                                  1;
98
```

Search completed: July 24, 2003, 12:52:23 Job time: 6.86524 secs

۳

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 24, 2003, 12:46:04; Search time 8.6358 Seconds (without alignments)
1959.945 Million cell updates/sec

Title: US-09-884-319A-2
Perfect score: 962
Sequence: 1 IPRVDLRVWQDCCEDCRTRG......VNIPGACCPVCLQKRAEEKP 176
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 283308 seqs, 96168682 residues
```

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0

283308

RESULT 1 S46224

peroxidasin - fruit fly (Drosophila sp.)

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

: PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28			25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	ω	2	_	No.	Result
102	102	102.5	103.5	104	104	105	105.5	106	107	107	108	108	109	111	113	123.5	125	125	132.5	134.5	134.5	137	139	139.5	147	147	148	153.5	Score	
10.6		•	•		10.8		11.0	11.0	11.1	11.1	11.2	11.2	11.3	11.5	11.7	12.8	13.0		13.8	14.0	14.	14.	14.	14.5	15.	15.3	15.4	16.0	Match	Query
1464	98	3133	194	886	615	884	1487	1038	.1464	153	1466	835	1486	1492	206	1496	1170	1170	1497	1822	810	1376	1172	3198	1172	941	1178	1535	Length	
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S59856	I49562	S52093	T14746	150694	A05269	T18649	B41182	T13177	CGHU1S	A27179	CGHU7L	JP0076	B40333	A40333	S18250	CGHU2V	A40558	TSHUP1	I49607	S63985	T10756	S63986	A42587	A43426	TSHUP2	A55195	A39804	S46224	ID	
	ĕ	S	н		alpha	ical pr	lagen alpha	ein - f			pha	ein - c	alpha	alpha	alpha	collagen alpha 2(V	thrombospondin 1	thrombospondin 1 p	procollagen type V	collagen alpha 2 c	Ō	ر.		collagen alpha 2 f	thrombospondin 2 p		thrombospondin pre		Description	

ALIGNMENTS

	A; Status: preliminary	
	J. Biol. Chem. 266, 8039-8043, 1991 J. Biol. Chem. 266, 8039-8043, 1991 A:Title: Cloning and sequencing of Chicken thrombospondin. A:Reference number: a19804 wHID: 91717056 DMTD: 2022631	
	C;ACCession: A39804 R:Lawler, J.; Duquette, M.: Ferro, P.	
	C:Species: Gallus gallus (chicken) C:Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999	
	RESULT 2	
	Db 1505 EVSCPPGVDPLTASGGLLP 1523	
	Qy 150 PATCAVPVNIPGACCP 165	
	Db 1445 VAQVVQLAAAPPQLVSKPKRSHCVDDKGTTRLNNEVWSPDVCTKCNCFHGQVNCLRERCG 1504	
	Qy 105SRLSTTECVDAGGESHANNTKWKKDACTICECKDGQVTCFVEACP 149	
	Db 1385 NDEVATAESYDSPLESLYDVNEERVSGLEELIGSFQKELKKLHKKLRKLEDSCNSADSEP 1444	
	Qy 60 GEHLSNSTSAFSTRSDASGTNDFREFVLEMQKTITDLRTQIKKLE 104	
	Db 1345 INLYLWQECGRCNSPPAIFVPTYRKPT-PSGDRQKRDLGKE 1384	
	Qy 4 VDLRVWQDCCEDCRTRGQFNAFSYHFRGRRSLEFSYQEDKPTKKTRPRKIPSVGRQ 59	
	Query Match 16.0%; Score 153.5; DB 2; Length 1535; Best Local Similarity 23.6%; Pred. No. 0.00011; Matches 47; Conservative 27; Mismatches 68; Indels 57; Gaps 7;	
ıl hom	C;Superfamily: peroxidasin; myeloperoxidase homology; proteoglycan amino-terminal F;19-44/Domain: proteoglycan amino-terminal homology <pah4> F;661-1350/Domain: myeloperoxidase homology <mpx></mpx></pah4>	
	A;Title: Peroxidasin: a novel enzyme-matrix protein of Drosophila development. A;Reference number: S46224; MUID:94341255; PMID:8062820 A;Accession: S46224	
7.; Pa	R;Nelson, R.E.; Fessler, L.I.; Takagi, Y.; Blumberg, B.; Keene, D.R.; Olson, P.F.; EMBO J. 13, 3438-3447, 1994	
	<pre>C;Species: Drosophila sp. C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Oct-2000 C:Accession: S46224</pre>	

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thrombospondin 2 precursor - human C;Species: Homo sapiens (man) C;Date: 19-May-1995 #sequence_revision C;Accession: A47379; A42173 R;LABBALL, T.L.; Byers, P.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:L35764; NID:g603944; PIDN:AAC42222.1; PID:g603945 C;Superfamily: chordin; von Willebrand factor type C repeat homology F:42-119/Domain: von Willebrand factor type C repeat homology <VWCl> F:692-753/Domain: von Willebrand factor type C repeat homology <VWCl> F:770-840/Domain: von Willebrand factor type C repeat homology <VWCl> F:858-922/Domain: von Willebrand factor type C repeat homology <VWCl> F:858-922/Domain: von Willebrand factor type C repeat homology <VWCl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chordin precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
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A55195
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A; Title: Xenopus chordin:
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A; Residues: 1-1178 <LAW>
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A; Residues: 1-941 <SAS>
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    Genomics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y.; Lu, B.; Steinbeisser, H.; Geissert, 779-790, 1994
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                                                                                                                                                                                                                                       SQPVHLPDQCCPVCEEKKEMREVKKP 762
                                                                                                                                                                                                                                                                               AVPVNIPGACCPVCLQK---RAEEKP 176
                                                                                                                                                                                                                                                                                                                                                                                                                KLNPR------GEIRGQIHIPNSCES----GGVSLTPEEPEYEYEIYEEGRQRDPDDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                             KTRPRKIPSVGRQGE-----HLSNSTSAFSTRSDASGTNDFREFVLEM-----QKTITDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KTEKKAEFCDRSCEELGTMFTELTGLRIVVNNLADNLQKVSEENQIMWELIGPNKTLKNQ
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                                                                                                                                                                                                                                                                                                                                                                    RTQIKKLESRLSTTECVDAGGESHANNTKWKKD---ACTICECKDGQVTCFVEACPPATC
Byers, F...
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26.0%;
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29.5%;
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Pred. No. 0.00025;
                                                                                                                                                                                                                                                                                                                            -GQLRAHGSRWAPDYDRKCSVCSCQKRTVICDPIVCPPLNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 147; DB 1; Pred. No. 0.00025;
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                                                                        03-Aug-1995 #text_change 13-Aug-1999
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ρ

REFVLEMQKTITDLRTQIKKLESRLSTTECVDAG--

GESHANNTKWKKDACTI 133

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A; Note: sequence extracted from NCBI backbone (NCBIP:111965)
C; Superfamily: unassigned collagens; fibrillar collagen carboxyl-terminal
F;48-106/Domain: von Willebrand factor type C repeat homology < VWC>
                                                                                                                                                                                                                                                                                                                      A; Title: Novel amino-terminal propertide configuration in a fibrillar A; Reference number: A43426; MUID:92381062; PMID:1380962 A; Accession: A43426
                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: A43426
R; Exposito, J.Y.; D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    collagen alpha 2 fibrillar chain precursor - sea urchin (Strongy C;Species: Strongylocentrotus purpuratus (purple urchin) C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
A43426
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F;652-691/Domain: EGF homology <EGF2
F;652-691/Domain: EGF homology <EGF2
F;928-930/Region: cell attachment (R-G-D) motif
F;151,316,330,457,584,710,1069/Binding site: carbohydra'
F;167-226/Disulfide bonds: #status predicted
F;167-270/Disulfide bonds: interchain #status predicted
F;612/Modified site: erythro-beta-hydroxyasparagine (Ass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;19-1172/Product: thrombospondin 2 **status predicted <MAT> F;319-377/Domain: von Willebrand factor type C repeat homology F;380-431/Domain: thrombospondin type 1 repeat homology <THR1> F;380-492/Domain: thrombospondin type 1 repeat homology <THR2> F;493-549/Domain: thrombospondin type 1 repeat homology <THR3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Description: participates in cell migration and adhesion, and in platelet aggregati C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; C;Keywords: beta-hydroxyasparagine; calcium binding; cell adhesion; glycoprotein; tri E;1-18/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: 6q27-6q27
C; Complex: homotrimer, disulfide linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R:LaBell, T.L.; Milewicz, D.J.; Genomics 12, 421-429, 1992
A;Title: Thrombospondin II: part A;Reference number: A42173; MUII
A;Accession: A42173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Sequence and characterization of the complete human A;Reference number: A47379; MUID:94010892; PMID:8406456 A;Accession: A47379 A;Molecule type: mRNA A;Residues: I-1172 <LAB> A;COSS-Teferences: GB:L12350; NID:9307505; PIDN:AAA03703.1; R;LaBell, T.L.; Milewicz, D.J.; Disteche, C.M.; Byers, P.H.
                                                                                                        F;48-106/Domain: von Willebrand factor type C repeat homology <VWC F;2978-3198/Domain: fibrillar collagen carboxyl-terminal homology
                                                                                                                                                                                                                                            A; Molecule type: nucleic acid
A; Residues: 1-3198 <EXP>
                                                                                                                                                                                                                                                                                                                                                                                                       J. Biol. Chem. 267, 17404-17408, 1992
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A;Experimental source: fibroblast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 560-1172 <LA2>
                                                                                                                                                                                                                                                                                                  A;Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Note: sequence extracted from NCBI backbone
                                                                                                                                                                                                                   A;Cross-references: GB:M92041; NID:g161448; PIDN:AAA30040.1; PID:g161449
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25; Conserv
  29;
                         Similarity
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48.1%;
                         14.5%;
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  15;
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                         Pred.
                                                  Score 139.5;
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Pred. No. 0.0003;
  Mismatches
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                            .0032;
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collagen alpha 5 chain - sea urchin (Strongylocentrotus purpura C; Species: Strongylocentrotus purpuratus (purple urchin) C; Date: 20-Jul-1996 #sequence_revision 08-Nov-1996 #text_change C; Accession: S63986; S64638

R; Exposito, J.Y.; Boute, N.; Deleage, G.; Garrone, R.
Eur. J. Biochem. 234, 59-65, 1995
A; Title: Characterization of two genes coding for a similar fou A; Reference number: S63985; MUID:96096722; PMID:8529669
A; Accession: S63986
A; Status: nucleic acid sequence not shown
A; Residues: 1-1376 <EXP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M64866; NID:g201994; PIDN:AAA40432.1; PID:g201995 C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 reper C;Keywords: calcium binding; glycoprotein F;319-377/Domain: von Willebrand factor type C repeat homology <VWC> F;380-431/Domain: thrombospondin type 1 repeat homology <THR1> F;436-492/Domain: thrombospondin type 1 repeat homology <THR2> F;435-492/Domain: thrombospondin type 1 repeat homology <THR3> F;435-588/Domain: EGF homology <EGF1> F;553-588/Domain: EGF homology <EGF1> F;652-691/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
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                                                                                                                                                                                                                                                                                                                                                                                              RESULT
S63986
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A;Recession: A39851
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-873 <BOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:L07803; GB:M87275; NID:g340421; PIDN:AAA53064.1; PID:g567241 A;Note: sequence extracted from NCBI backbone (NCBIP:81502) R;Bornstein, P.; O'Rourke, K.; Wikstrom, K.; Wolf, F.W.; Katz, R.; Li, P.; Dixit, V J. Biol. Chem. 266, 12821-12824, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: Characterization of mouse thrombospondin 2 sequence A; Reference number: A42587; MUID:92147683; PMID:1371115 A; Accession: A42587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, J. Biol. Chem. 267, 3274-3281, 1992
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A; Reference :
                                           A;Cross-references: EMBL:X89804 R;Exposito, J.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: nucleic acid
A; Residues: 1-1172 <LAH>
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Best Local (
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  number:
the EMBL Data number: S64637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NTKWKKDACTICECKDGQVTCFVEACPPATCAVPVNIPGACCPVC 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CECKDGQVTCFVEACPPATCAVPVNIPGACCPVC 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NETWVVDSCTTCTCKKFKTVCHQITCSPATCANPSFVEGECCPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EFVLEMQKTITDLRTQIKKLESRL--
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                                                                                                                                                                                                                                                                                                                                                               5 chain - sea urchin (Strongylocentrotus purpuratus) (fragment)
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28.6%;
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No. 0.0014;
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                                           A; Molecule type: A; Residues: 1-38
                                                                                                                   submitted to the EMBL Data A; Reference number: S64637
                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-1822 <
                                                                                                                                                                                                                                                                                       A;Title: Characterization of two genes coding for a sim A;Reference number: S63985; MUID:96096722; PMID:8529669 A;Accession: S63985
                                                                                                                                                                                                                                                                                                                                                                  R; Exposito, J.Y.; Boute, N.; Deleage, G.; Eur. J. Biochem. 234, 59-65, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                collagen alpha 2 chain precursor - sea urchin (Strongylocentrotus purpuratus) C;Species: Strongylocentrotus purpuratus (purple urchin) C;Date: 20-Jul-196 #sequence_revision 01-Nov-1996 #text_change 23-Aug-1997 C;Accession: S63985; S64637
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A; Residues: 1-810 < KUR>
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                                                                                              A; Accession:
                                                                                                                                                                    R; Exposito, J.Y
                                                                                                                                                                                             A; Cross - references:
                                                                                                                                                                                                                                                                   A; Status: nucleic acid sequence
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                       :Cross-references:
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                                                                                            number: s64637
                                         rype: DNA
1-381,'DT',384-677,'N',679-1010,'L',1012-1822
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                       EMBL: X89806
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Garrone,

a similar

four-cysteine motif of th

(fragme

July 1995

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A;Introns: 73/1; 136/2; 221/1; 369/1; 517/1; 659/1; 799/1; 948/1; C;Superfamily: von Willebrand factor type C repeat homology C;Keywords: extracellular matrix F;15-73/Domain: von Willebrand factor type C repeat homology <VWC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-658,'G',660-870,'G',872-901,'H',903-1185,'T',1187-1214,'Y',1216-1376
A;Cross-references: EMBL:X89804
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                          A;Description: Protein kinase C-binding A;Reference number: 217122
                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Kuroda, S.; Tokunaga, C.; Kiyohara, Y.; Konishi, submitted to the EMBL Data Library, November 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999 C;Accession: T10756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Accession: S64638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 GESHANNTKWKKDACTICECKDGQVTCFVEACPPATCAVPVNIPGACCPVC 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Norway
KSGAVECRRMSCPPLNCSPDSLPVHISGQCCKVCRPK 334
                           KDGQVTCFVEACPPATC---AVPVNIPGACCPVCLQK
                                                                                   GIMDLQELLAKMTAKLNYAETRLGQLENCHCEKTC - QVSGLLYRDQDSWVDGDNCGNCTC
                                                                                                                            GTNDFREFVLEMQKTITDLRTQIKKLESRLSTTECVDAGGESHANNTKW-KKDACTICEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GIPYLHGEEWKVDECTTCACDNATTTCVIESCQPAFCAEPIKPEGECCFLC 70
                                                                                                                                                                                                                                                           source: strain Sprague-Dawley, brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                 EMBL:U48246; NID:g3851179; PID:g3851180
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41.2%;
                                                                                                                                                                                           14.0%;
                                                                                                                                                                       Score 134.5;
Pred. No. 0.00
14; Mismatches
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Pred. No. 0.0023;
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                                                                                                                                                                                       134.5; DB 2;
No. 0.0022;
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C;Species: Homo sapiens (man)
C;Date: 23-Aug-1987 #sequence_revision 03-Aug-1995 #text_change 17-Nov-2000
C;Date: A26155: A34274; A30140; A25812; A05172; A42927
                                                                                                                               J. Biol. Chem. 264, 11222-11227, 1989
A; Title: Characterization of the promoter region of the human A; Reference number: A34274; MUID:89291870; PMID:2544587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      맑
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology: F;39-98/Domain: von Willebrand factor type C repeat homology <VWC> F;1270-1497/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dev. Dyn. 195, 113-120, 1992
A;Title: Localization of pro-alpha 2(V) collagen transcripts
A;Reference number: 149607; MUID:93214071; PMID:1297453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   procollagen type V alpha 2 - mouse C; Species: Mis missing.
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A;Cross-references: GB:J04835
R;Hennessy, S.W.; Frazier, B.A.;
J. Cell Biol. 108, 729-736, 1989
                                                               A; Molecule type: DNA
A; Residues: 1-166 <LAH>
                                                                                                                                                                                                                                                                                                             A;Title: The structure of human thrombospondin, an adhesive glycoprotein with multiple A;Reference number: A26155; MUID:87057617; PMID:2430973 A;Accession: A26155
                                                                                                                                                                                                                                                                                                                                                                             R;Lawler, J.; Hynes, R.O.
J. Cell Biol. 103, 1635-1648, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thrombospondin 1 precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: Col5a-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-1497 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A; Accession: I49607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Andrikopoulos,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: I49607
                                                                                                               A;Accession: A34274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 C 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 C 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 GQMYLNRDIWKPSPCQICVCDNGAILCDKIECPEVLNCANPITPPGECCPVCPQ 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K.; Suzuki, H.R.; Solursh, M.; Ramirez,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GB:L02918; NID:g309180; PIDN:AAA37440.1; PID:g309181
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41.0%;
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                    Kim,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 132.5; DB 2;
Pred. No. 0.0058;
Pred. No. 0.0058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 134.5; DB 2;
Pred. No. 0.0048;
5; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; 395/1; 460/3; 534/1; 678/1; 743/3 817/1; 965/1; von Willebrand factor type C repeat homology
                      D.D.; Deckwerth,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1822;
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                    T.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                      Baumgartel,
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                                                                                                                                                      thrombospondin
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                                                                                                                                                                                                                      protein,
                      D.M.;
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                      Rotwein,
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thrombospondin
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12

ب

precursor

mouse

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A;Residues: 1-83,'A',85-522,'A',524-1170 <HEN>
A;Cross-references: EMBL:X14787; NID:937464; PIDN:CAA32889.1; PID:937465
A;Note: parts of this sequence, including the amino end of the mature protein, R;Kobayashi, S.; Eden-McCutchan, F.; Framson, P.; Bornstein, P.
Biochemistry 25, 8418-8425, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Disulfides modulate RGD-inhibitable cell adhesive activity of thrombospondin A;Reference number: A42927; MUID:92348511; PMID:1379247 A;Accession: A42927
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A;Cross-references: GDB:120438;
A;Map position: 15q15-15q15
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                                                                                                                                                                                                                                                                                                                                                                                 F;270,274/Disulfide bonds: interchain *status predicted F;610/Modified site: erythro-beta-hydroxyasparagine (Asn) *status F;1051/Binding site: carbohydrate (Asn) (covalent) *status absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;926-928/Region: cell attachment (R-G-D) motif
F;171-232/Disulfide bonds: #status predicted
F;171-33/Disulfide bonds: #status predicted
F;248.360,708,1667/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;650-689/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Description: participates in cell migration and adhesion, and in platelet aggregati C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; C;Keywords: beta-hydroxyasparagine; calcium binding; cell adhesion; glycoprotein; tri E;1-18/Domain: signal sequence #status predicted <SIG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Note: the list of introns may be incomplete C; Complex: homotrimer, disulfide linked
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Note: Cys-992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Cross-references: GB:M14326; NID:g340005; PIDN:AAA61237.1; PID:g553801
A,Note: parts of this sequence, including the amino end of the mature protein,
R;Sun, X.; Skorstengaard, K.; Mosher, D.F.
J. Cell Biol. 118, 633-701, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-83,'A',85-374,'RC' <DIX>
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A; Residues: 1-83, 'A', 85-397 < KOB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type:
                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                          Local Similarity
348
                                                            143 CFVEACPPATCAVPVNIPGACCPVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A30140
CKKVSCPIMPCSNATVPDGECCPRC
                                                                                                                            RTIVTTLQDSIRKVTEENKELANELRRPPLCYHNGVQYRNNEEWTVDSCTECHCQNSVTI 347
                                                                                                                                                                                        REFVLEMQKTITDLRTQIKKLESRLSTTECVDAGGESHANNTKWKKDACTICECKDGQVT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is shown
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                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thrombospondin type 1 repeat homology <THR1>
thrombospondin type 1 repeat homology <THR2>
thrombospondin type 1 repeat homology <THR3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thrombospondin 1 #status predicted <MAT>
von Willebrand factor type C repeat homology <VWC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGF homology <EGF1>
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                                                                                                                                                                                                                                                           13;
                                                                                                                                                                                                                                                                                          Score 125; DB 1; Pred. No. 0.019;
                                                                                                                                                                                                                                                           Mismatches
372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homology <THR2>
                                                                                                                                                                                                                                                           47;
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A; Residues: 1-1170 <LAW>
A; Residues: 1-1170 <LAW>
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A; Residues: 1-1170 <LAW>
A; Cross-references: GB:M62449; GB:M62450; GB:M62451; GB:M62452; GB:M62453; GB:M62465; GB:M62466; GB:M62467; GB:M62468; GB:M62469; NID:9511867; MS:M62465; GB:M62466; GB:M62467; GB:M62468; GB:M62469; NID:9511867; R; Bornstein, P.; Alfi, P.; Devarayyalu, S.; Framson, P.; Li, P.

J. Biol. Chem. 265, 16691-16698, 1990
A; Title: Characterization of the mouse thrombospondin gene and evaluation on A; Reference number: A37905; MUID:90375546; PMID:2398070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Molecule type: protein
A;Rosidoues: 19-26,'X',28-37 <CHE>
C;Complex: homotrimer, disulfide linked
C;Complex: homotrimer disulfide linked
C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology;
C;Keywords: calcium binding; glycoprotein; homotrimer
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-1170/Product: thrombospondin 1 #status predicted <MAT>
F;317-375/Domain: von Willebrand factor type C repeat homology <THR1>
F;378-429/Domain: thrombospondin type 1 repeat homology <THR2>
F;434-490/Domain: thrombospondin type 1 repeat homology <THR3>
F;491-547/Domain: thrombospondin type 1 repeat homology <THR3>
F;491-547/Domain: EGF homology <EGF>
F;248,360,708,1067/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Date: 05-Jun-1992 #sequen
C;Accession: A40558; A3790:
R;Lawler, J.; Duquette, M.
Genomics 11, 587-600, 1991
C; Species: Homo sapiens (man)
C; Date: 31-Jul-1989 #sequence_revision 28-Jul-1995 #text_change 31-Dec-2000
C; Date: 31-Jul-1989 #sequence_revision 28-Jul-1995 #text_change 31-Dec-2000
C; Accession: A31427; A54555; S43643; A25874; I55239; I59025; A25374; A30017
R; Woodbury, D.; Benson-Chanda, V.; Ramirez, F.
J. Biol. Chem. 264, 2735-2738, 1989
A; Title: Amino-terminal propeptide of human pro-alpha2(V) collagen conforms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:J05605; GB:J05606; NID:g201991; PIDN:AAA40431.1; PID:g554390 R;Laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M. J. Biol. Chem. 267, 3274-3281, 1992
A;Title: Characterization of mouse thrombospondin 2 sequence and expression during (A;Reference number: A42587; MUID:92147683; PMID:1371115
A;Status: Preliminary; not compared with conceptual translation
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A;Molecule type: DNA
A;Residues: 1-490 <BOR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Chen, H.; Aeschlimann, D. FEBS Lett. 387, 36-41, 1996
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A; Residues: 1-1152, 'P', 1154-1170 <LAH>
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29.4%;
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C; Comment: The a C; Genetics:
A; Gene: GDB: COL!
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A; Residues: 398-1496 <WEI>
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A; Residues: 1-32 <GRE>
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A; Residues: 1002-1226 < RE2>
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A;Residues: 1003-1034 <RES>
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A;Experimental source: rhabdomyosarcoma cell line R;Myers, J.C.; Loidl, H.R.; Stolle, C.A.; Seyer, J.M.
J. Biol. Chem. 260, 5533-5541, 1985
A;Title: Partial covalent structure of the human alpha 2 type A;Reference number: I55239; MUID:85182703; PMID:2985598
A;Accession: I55239
A;Katric terror
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Nucleic Acids Res. 15, 181-198, 1987
A;Title: The pro alpha 2(V) collagen gene is evolutionarily A;Reference number: A25874; MUID:87146331; PMID:3029669
A;Accession: A25874
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J. Biol. Chem. 260, 11216-11222, 1985
A;Title: Complete primary structure of the human alpha-2
A;Reference number: A25374; MUID:85289337; PMID:2411731
A;Accession: A25374
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                                            A;Note: the authors translated the codon GAA for residue C;Comment: Prolines and lysines at the third position of are 5-hydroxylated and subsequently O-glycosylated.
                                                                                                                                                          A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1449-1463, 'E', 1465-1495, 'A' <TSI>
A; Residues: 1449-1463, 'E', 1465-1495, 'A' <TSI
A; Residues: 1449-1463
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A;Title: Genetic distance of two fibrillar collagen loci, COL3A1 and COL5A2, locat A;Reference number: A30017; MUID:89138450; PMID:3224983
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A; Reference number: A54555; MUID:92314691; PMID:1820205
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A; Residues: 1227-1417, 'T',1419-1437, 'S',1439-1496 <MYE>
A; Cross-references: GB:M11718; NID:g180912; PIDN:AAA520
A; Experimental source: normal fibroblasts
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amino-terminal propeptide domain appears not to be completely cleaved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PMID: 2914927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIDN: AAA52058.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G.G.
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                                                                                                   8.1; PID:g179696
1460 as Gln, and GAG
the tripeptide repeat
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, M.F.; Boutillon,
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                                                                                                   nd GAG for repeating
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F;941-943/Region: Cell attachment (R-G-D) motif
F;1064-1066/Region: cell attachment (R-G-D) motif
F;1067-1069/Region: cell attachment (R-G-D) motif
F;1097-1099/Region: cell attachment (R-G-D) motif
F;1097-1099/Region: cell attachment (R-G-D) motif
F;1133-1135/Region: cell attachment (R-G-D) motif
F;1133-1135/Region: carboxyl-terminal nonhelical telopeptide
F;1251-1269/Region: carboxyl-terminal propeptide #status predicted <CPP>
F;1259-1496/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
F;27/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;193-194/Cleavage site: Ala-Gln (procollagen N-endopeptidase) #status predicted
F;291/Modified site: allysine (Lys) #status predicted
F;290,139/Modified site: 5-hydroxylysine (Lys) #status predicted
F;299,139/Modified site: 5-hydroxylysine (Lys) #status predicted
F;1025-Modified site: carbohydrate (Lys) (covalent) #status predicted
F;1259,139/Modified site: carbohydrate (Lys) #status predicted
F;1259,139/Modified site: carbohydrate (Lys) #status predicted
F;1259,139/Modified site: carbohydrate (Asn) (covalent) #status predicted
F;1259,139/Modified site: carbohydrate (Asn) (covalent) #status predicted
F;1259,139/Modified site: carbohydrate (Asn) (covalent) #status predicted
F;1333-1494,1407-1491;fide bonds: #status predicted
F;1333-1494,1407-1491;fide bonds: #status predicted
C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; C;Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein F;1-25/Domain: signal sequence #status predicted <SIG> F;26-184/Domain: amino-terminal propeptide #status predicted <PRO> F;36-95/Domain: von Willebrand factor type C repeat homology <VWC> F;36-95/Domain: von Collagen alpha 1(II) chain (fragment) #status predicted <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biol. Chem. 266, 23446-23402, 1991
A;Title: Type II collagen mRNA containing an alternatively spliced
A:Reference number: S18250; MUID:92078225; PMID:1744138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Date: 22-Nov-1993 #sequence_revision
C;Accession: S18250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          collagen alpha 1(II) chain precursor - chicken (fragment)
C; Species: Gallus gallus (chicken)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 2q31-2q31
A; Introns: 33/1; 812/3; 8
                                                                                                                                                                                                                                                  A; Gene:
                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-206 < NAH>
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J. Bïol. Chem. 266, 23446-23452, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Function:
                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:M74435; NID:g211635; PIDN:AAA48714.1; PID:g211636
                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: S18250
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;27-1250/Product: collagen alpha 2(V) chain #status predicted <MAT>
;27-193/Domain: amino-terminal propeptide (uncleaved) #status predi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: may play a role in controlling the lateral growth of collagen I fibrils superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology, superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology, superfamily: colled coll; extracellular matrix; glycoprotein; hydroxylysine; hydroxyprol
                                                                                                                                                                                                                                                                               Genetics:
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42.6%;
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5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-Jul-1996 #text_change 13-Aug-1999
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A;Note: this sequence is presented as substitutions relative to another sequence es they replace; the appropriate interpretation of the sequence figure was recc;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal C;Keywords: collade coll; extracellular matrix; glycoprotein; trimer; triple hel F;37-99/Domain: von Willebrand factor type C repeat homology <VWC>F;1263-1492/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-1492 <SUA>
A; Cross-references: GB: M63596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Cell Biol. 115, 565-575, 1991
A;Title: Expression of two nonallelic type
A;Reference number: A40333; MUID:92011898;
A;Accession: A40333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: A40333
R; Su, M.W.; Suzuki, H.R.; Bieker, J.J.; Solursh,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Species: Xenopus laevis (African claw C; Date: 16-Sep-1992 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         collagen alpha 1'(II) chain precursor - African clawed frog
C; Species: Xenopus laevis (African clawed frog)
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Search completed: July 24, 2003, 12:53:41 Job time: 9.6358 secs
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                                                                                                                                                                                                                                                                           Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 CVDAGGESHANNTKWKKDACTICECKDGQVTCFVEAC-PPATCAVPVNIP-GACCPVC
                                                                                                                              163 CCPVC 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus
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                                                                                                                                                                      30 EDVLDTGSCVQ-DGQRYSDKDVWKPEPCQICVCDTGTVLCDEIICEESKDCPNAEIPFGE 88
                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                     Similarity 35.
                                                                                      CCPIC
                                                                                                                                                                                                             ESRLSTTECVDAGGESHANNTKWKKDACTICECKDGQVTCFVEACPPATCAVPVNIP-GA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CVQ-DGQSYSDKDVWKPEPCRICVCDTGTVLCDEIICEEPQDCPSP-EIPFGECCPVC
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43.1%;
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Pred. No. 0.035;
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Pred. No. 0.
                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-Sep-1992
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                                                                                                                                                                                                                                                                                               DB 2; Length 1492;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ຸນ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence in
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Result
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1: /cgn2_6/ptodata/2/paa/PcT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/Us06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/Us08_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/Us08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/Us08_NEW_COMB.pep:*

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PCT-US02-18638A-36
US-10-249-686-2
US-10-273-573-5521
US-10-464-368-58
US-10-464-368-59
US-10-464-368-54
US-10-464-368-54
US-10-464-368-57
PCT-US03-12521-2
PCT-US03-1253B-46
US-10-464-368-55

US-10-451-689-1

US-10-451-689-3

US-10-273-573-5790

US-10-273-573-9184

US-10-273-573-6705

US-10-273-573-6767

US-10-464-368-63

US-10-273-573-6812

US-10-273-573-6812

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US-10-273-573-6812
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US-10-450-186-41
PCT-US00-28803-4
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330.094 Million cell updates/sec
                                                                                                 Sequence 28, Appli Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 55, Appli Sequence 58, Appli Sequence 56, Appli Sequence 54, Appli Sequence 54, Appli Sequence 57, Appli Sequence 570, Appli Sequence 570, Appli Sequence 570, Appli Sequence 570, Appli Sequence 574, Appli Sequence 574, Appli Sequence 5750, Appli Sequence 5750, Appli Sequence 5767, A
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                                                     Sequence
Sequence
     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to have a being printed,
                              6812, Ap
7259, Ap
                                                                              63, Appl
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27
65	65	65	65	65	65	65	65		65		65.5		66	66	66	67	67	67.5
o. 8	6.8	6.8	6.8	6.8	6.8	6.8	6.8	6.8	6.8	6.8	6.8	6.8	6.9	6.9	6.9	7.0	7.0	7.0
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US-10-374-979-4	US-10-374-979-3	US-10-464-368-82	US-10-464-368-81	US-10-273-573-10236	US-10-273-573-10235	US-10-273-573-10011	US-10-273-573-10007	US-10-464-368-95	US-10-411-910A-76	US-10-370-481-35	US-60-470-920-38	US-60-479-073-287	US-10-287-971-389	US-09-291-417D-151	US-10-451-901-10	US-10-411-910A-6	US-10-273-573-5752	US-10-343-063A-23
4	Sequence 3, Appli	Sequence 82, Appl	Sequence 81, Appl	Sequence 10236, A	Sequence 10235, A	Seguence 10011, A	Sequence 10007, A	Sequence 95, Appl	Sequence 76, Appl	Sequence 35, Appl	Sequence 38, Appl	Sequence 287, App	Sequence 389, App	•	Sequence 10, Appl	Sequence 6, Appli	Sequence 5752, Ap	Sequence 23, Appl

ALIGNMENTS

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RESULT 1
US-10-331-496A-28
                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/331,496A CURRENT FILING DATE: 2002-12-30

PRIOR APPLICATION NUMBER: US 60/345,444

PRIOR ETLING DATE: 2002-01-02

PRIOR FILING DATE: 2002-01-05

PRIOR PPLICATION NUMBER: US 60/361,885

PRIOR APPLICATION NUMBER: US 60/360,066

PRIOR FILING DATE: 2002-02-25

PRIOR PILING DATE: 2002-03-05

PRIOR APPLICATION NUMBER: US 60/362,004

PRIOR APPLICATION NUMBER: US 60/366,869

PRIOR APPLICATION NUMBER: US 60/366,869

PRIOR APPLICATION NUMBER: US 60/366,869

PRIOR FILING DATE: 2002-03-02
                                                                                            US-10-331-496A-28
                                                                                                                                    NUMBER OF SE
SEQ ID NO 28-
LENGTH: 149
TYPE: PRT
Query Match
Best Local Similarity
Matches 176; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 28, Application US, GENERAL INFORMATION:
APPLICANT: FRANTZ, GRETCHEN
                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/404,809
PRIOR FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: US 60/405,645
PRIOR FILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: WU, THOMAS D.
APPLICANT: ZHANG, ZEML
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF TUMOR
FILE REFERENCE: P5014R1-PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 2002-03-28
                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/366,284 PRIOR FILING DATE: 2002-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                              ORGANISM: Homo sapien
                                                                                                                                                        1496
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PHILLIPS, HEIDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPENCER, SUSAN D. WILLIAMS, P. MICKEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/10331496A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLAKIS, PAUL
      100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                                                                                                                             R: US 60/404,809
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        0;
      Score 962; DB 6;
Pred. No. 7.9e-89;
Mismatches 0;
                                                Length 1496;
        Indels
        0,
        Gaps
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1 IPRVDLRVWQDCCEDCRTRGQFNAFSYHFRGRRSLEFSYQEDKPTKKTRPRKIPSVGRQG

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RESULT 3 .
PCT-US00-28803-4
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US-10-450-186-41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         '; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7486326CD1
US-10-450-186-41
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Sequence 4, Application PC/TUS0028803 GENERAL INFORMATION:
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Best Local S
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PRIOR FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: US 60/257,852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PCT/US01/48517
PRIOR FILING DATE: 2001-12-12
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CURRENT FILING DATE: 2003-06-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 915
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APPLICATION NUMBER: US 60/265,926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/263,096 FILING DATE: 2001-01-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/262,932
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APPLICATION NUMBER: US 60/260,105
FILING DATE: 2001-01-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/263,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1441 ANNTKWKKDACTICECKDGQVTCFVEACPPATCAVPVNIPGACCPVCLQKRAEEKP 1496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1321 IPRVDLRVWQDCCEDCRTRGQFNAFSYHFRGRRSLEFSYQEDKPTKKTRPRKIPSVGRQG 1380
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                                                                                                                                                                                                                              669 GOQRPHGARWAPNYDPLCSLCTCQRRTVICDPVVCPPPSCPHPVQAPDQCCPVCPEKQ 726
                                                                                                                                                                                                                                                                                                      117 GESHANNTKWKKD---ACTICECKDGQVTCFVEACPPATCAVPVNIPGACCPVCLQKR 171
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                                                                                                                                                                                                                                                                                                                                                                                 h 12.8%;
Similarity 34.5%;
20; Conservative 1
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YUE, Henry; DING, Li;
YUE, Henry; DING, Li;
LAL, Preeti G; LEE, Ernestine A;
RAMKUMAR, Jayalaxmi; THANGAVELU, Kavitha;
RAMKUMAR, Jayalaxmi; LEE, Sally;
RAMKUMAR, Jayalaxmi; LEE, Sally;
RAMKUMAR, Jayalaxmi; RAMKUMAR, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INCYTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/10450186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELLIOTT, Vicki S.; LU, Dyung Aina M.;
HAFALIA, April J.A.; AZIMZAI, Yalda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAWLA, Narinder K.; LU,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORPORATION; GRIFFIN,
                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 123.5; DB 6 Pred. No. 5.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                               RESULT 5
PCT-US02-18638A-36
Sequence 36, Application PC/TUS0218638A
; GENERAL INFORMATION:
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SEQ ID NO 2
LENCTH: 451
TYPE: PRT
                                                                                Matches
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Best Local
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                                                                                                                       Query Match
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                                                                              Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: PCT/US00/28803
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US 60/160,106
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US 60/162,547
PRIOR APPLICATION NUMBER: US 60/162,547
PRIOR FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 7
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APPLICANT: Zambrowicz, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: Novel Human Proteins and Polynucleotides
TITLE OF INVENTION: Encoding the Same
FILE REFERENCE: LEX-0070-PCT
CURRENT APPLICATION NUMBER: PCT/US00/28803
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US 60/160,106
PRIOR APPLICATION NUMBER: US 60/162,547
PRIOR APPLICATION NUMBER: US 60/162,547
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: Novel Human Proteins and Polynucleotides
TITLE OF INVENTION: Encoding the Same
FILE REFERENCE: LEX-0070-PCT
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nes 15; Conserv
                                      131 CTICECKDGQVTCFVEACPPATCAVPVNIPGACCPVCLQKRAEE 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 CVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQ 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 CTICECKDGOVTCFVEACPPATCAVPVNIPGACCPVCLQKRAEE 174
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CVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hilbun, Erin
                                                                                   Conservative
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                                                                                                      12.0%;
34.1%;
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                                                                                                      Score 115; DB 1; Pred. No. 0.00017;
                                                                                Mismatches
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                                                                                   19;
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                                                                                                                         Length 451;
                                                                                   Indels
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    181
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APPLICANT: Millennium Pharmaceuticals, Inc.

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RESULT 7
US-10-273-573-5521
Sequence 5521, Application US
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL M
FILE REFERENCE: 21272-066
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US-10-249-686-2
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US-10-249-686-2
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; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-USO2-18638A-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/10249686 GENERAL INFORMATION:
APPLICANT: Burchardt, Elmar Reinhold
                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local S
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CURRENT FILING DATE: 2003-04-30
PRIOR APPLICATION NUMBER: PCT/EP01/12663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Procollagen (III) Propeptides and Related Substances for Treatin TITLE OF INVENTION: Fibrotic Diseases FILE REFERENCE: ERB-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/335,936
PRIOR FILING DATE: 2001-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
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PRIOR APPLICATION NUMBER: US 60/298,159
PRIOR FILING DATE: 2001-06-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 141
                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                     111 ECVDAG----GESHANNTKWKKDACTICECKDGQVTCFVEACPPATCAVP-VNIP-GACC 164
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                                                                                                                                                                                                                           165 PVCLQ 169
                                                                                                                                                                                     63 AVCPQ 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 QVEGQDEDIPPITCVQNGLRYHDRDV-WKPEPCRICVCDNGKV-----LCDDVICDETKN
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                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                  Application US/10273573
                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-10-31
                                                                                                                                                                                                                                                                                                                                                                  10.9%;
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                       MACROPHAGE NUCLEIC
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                                                                                                                                                                                                                                                                                                                                             Score 105; DB 6;
Pred. No. 0.00044;
5; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 107; DB 1; Length 1464; Pred. No. 0.0044; Indels 18; Mismatches 31; Indels 1
                       ACIDS AND POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                  29;
                                                                                                                                                                                                                                                                                                                                                                                   Length 141;
                                                                                                                                                                                                                                                                                                                                                  Indels
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US-10-464-368-59
; Sequence 59, Application US/10464368
; GENERAL INFORMATION:
; APPLICANT: KrumLauf, Robb
; APPLICANT: Ellies, Debra
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US-10-464-368-58
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APPLICANT: Ellies, Debra
APPLICANT: Ellies, Debra
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
FILE REFERENCE: 40716-IP-017
CURRENT APPLICATION NUMBER: US/10/464,368
CURRENT FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/388,970
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 140
CONTENT SEQ ID NOS: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-273-573-5521
                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                      US-10-464-368-58
                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin
SEQ ID NO 58
LENGTH: 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 58, Application US/10464368 GENERAL INFORMATION:
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SOFTWARE: Custom
SEQ ID NO 5521
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Best Local :
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Best Local
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CURRENT FILING DATE: 2002-10-18
PRIOR RPPLICATION NUMBER: 09/522,929
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR FILING DATE: 2001-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (35)..(2402)
OTHER INFORMATION: von Willebrand factor type D domain identified by PFam,
OTHER INFORMATION: accession name vwd, E-value=1.7e-183, PFam score of 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (826)..(875)
OTHER INFORMATION: PRECURSOR GLYCOPROTEIN SIGNAL CELL domain identified OTHER INFORMATION: EMATRIX, accession number PD02576A, p-value=1.000e-40 OTHER INFORMATION: 27.60
                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                        ORGANISM: MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: DOMAIN LOCATION: (35)...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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                                                                                                                                                              108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25; Conserv
                                                                                                                                                                                                                                         Similarity
17; Conserv
                                                                                                                                                              GVIYRNGEKFEPNCQYFCTCRDGQIGCLPRCQLDVLLPGPDCPAPRKVAVPGECC
                                                                                                                                                                                                GESHANNTKWKKDACTICECKDGQVTCFVEA----CPPATCAVP--VNIPGACC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TQCIGEDGVQHQFLEAWVPDHQPCQICTCLSGRKVNCTTQPCPTAKAPTCGLCEVARLRQ 2614
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                                                                                                                                                                                                                                                                                                                                                                                                                     version 3.2
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27.5%;
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30.9%;
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Pred. No. 0.96;
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                                                                                                                                                                                                                                                                             DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FOR REGULATING BONE DEPOSITION
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; SOFTWARE: PatentIn v

; SEQ ID NO 56

; LENGTH: 347

; TYPE: PRT

; ORGANISM: RAT

US-10-464-368-56
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                                                                                                                                                                                                 Sequence 54, Application US/10464368 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local
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Best Local Similarity
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APPLICANT: Krumlauf, Robb
APPLICANT: Ellies, Debra
APPLICANT: Ellies, Debra
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATING BONE DEPOSITION
FILE REFERENCE: 40716-17-017
CURRENT APPLICATION NUMBER: US/10/464,368
CURRENT FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/388,970
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/464,368 CURRENT FILING DATE: 2003-06-16 PRIOR APPLICATION NUMBER: 60/388,970
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APPLICANT: Ellies, Debra

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATING BONE DEPOSITION
FILE REFERENCE: 40716-IP-017
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PRIOR APPLICATION NUMBER: 60/388,970
PRIOR FILING DATE: 2002-06-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.2
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CURRENT FILING DATE: 2003-06-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 CVDAG-----GESHANNTKWKKDACTICECKDGQVTCFVEAC-----PPATCAVP--VN 158
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                                                                                                                                                                                                                                                                                                                               154 LPGKCCEEWVC 164
                                                                                                                                                                                                                                                                                                                                                                       159 IPGACCP--VC 167
                                                                                                                                                                                                                                                                                                                                                                                                                 101 CVFGGSVYRSGESFQSSCKYQ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 81; DB 6; Pred. No. 0.32; 5; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                 -CTCLDGAVGC-VPLCSMDVRLPSPDCPFPRRVK 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
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; LENGTH: 348
; TYPE: PRT
; ORGANISM: MOUSE
US-10-464-368-54
; OTHER INFORMATION: Incyte ID No: 926296CD1 US-10-451-901-2
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Best Local S
Matches 25
                                                                                           SOFTWARE: PERL Program
SEQ ID NO 2
LENGTH: 995
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NUCLEIC ACID-ASSOCIATED PROTEINS FILE REFERENCE: PF-0869 USN CURRENT APPLICATION NUMBER: US/10/451,901 CURRENT FILING DATE: 2003-06-23 PRIOR APPLICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/10451901 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT/US01/50256
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: US 60/257,714
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: US 60/260,081
PRIOR FILING DATE: 2001-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                       NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/263,823
PRIOR FILING DATE: 2001-01-23
                                                                                                                                                                                           PRIOR FILING DATE:
                                                                                                                                                                                                             PRIOR APPLICATION NUMBER:
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                                                                       ORGANISM: Homo
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                                     NAME/KEY: misc_feature
                                                         FEATURE:
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nes 25; Conserv
                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/266,088 FILING DATE: 2001-02-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INCYTE CORPORATION; BAUGHN, Mariah R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LU, Dyung Aina M.; GANDHI, Ameena
GRIFFIN, Jennifer A.; XU, Yuming;
AZIMZAI, Yalda; GIETZEN, Kimberly
TANG, Y. Tom; WARREN, Bridget A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YANG, Junming; GORVAD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MASON, Patricia M.; BURFORD, Neil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRIBOULEY, Catherine M.; YUE, Henry;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAMKUMAR, Jayalaxmi; YAO, Monique G.; POLICKY, Jennifer L.; WALIA, Narinder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMERLING, Brooke M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Preeti G.; BOROWSKY, Mark L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sajeev; DING,
                                                                                                                                                                                           2001-10-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 81; DB 6 Pred. No. 0.33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MARQUIS, Joseph P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEE, Ernestine A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -CTCLDGAVGC-VPLCSMDVRLPSPDCPFPRRVK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anita;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ameena R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 6; Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ly J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
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Query Match Best Local Similarity

8.3%; 18.1%;

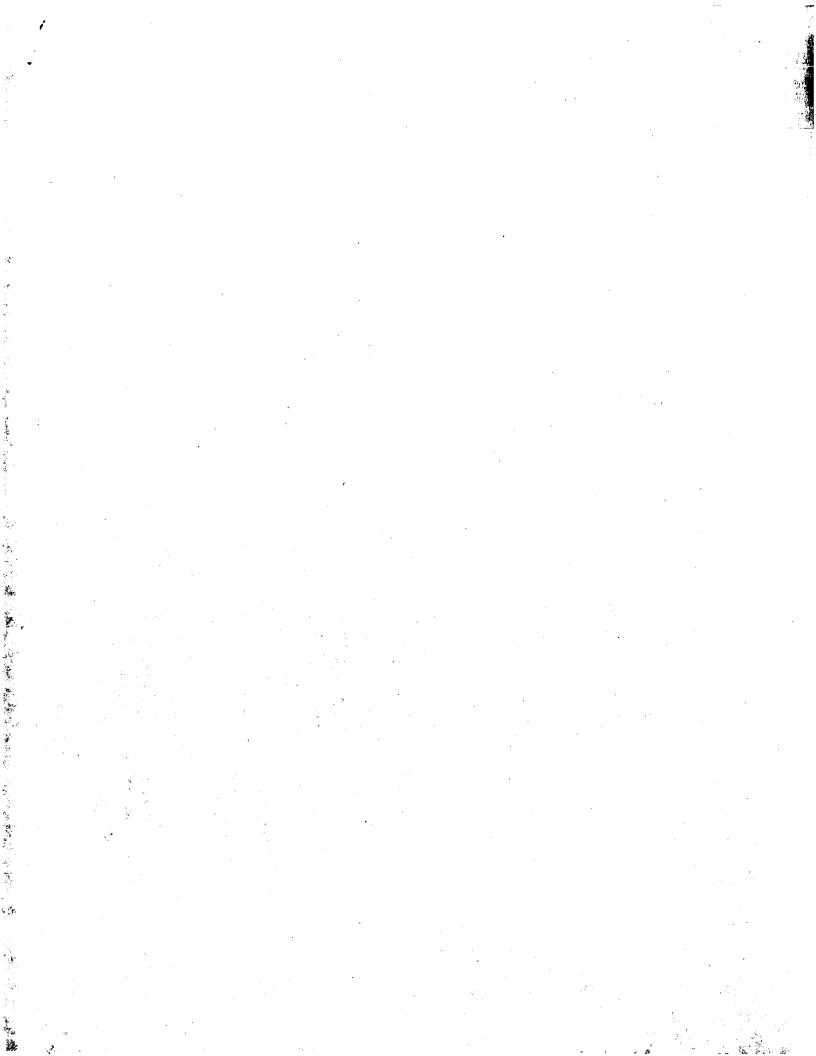
Score 79.5; Pred. No. 1

DB 6;

Length 995;

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; ORGANISM: BOVINE
US-10-464-368-57
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US-10-464-368-57
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GENERAL INFORMATION:
APPLICANT: Krumlauf, Robb
APPLICANT: Ellies, Debra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 57
LENGTH: 349
                                    SEQ ID NO 2
LENGTH: 349
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                                                                                                                                                       APPLICANT: Jacobson, Nasreen
APPLICANT: Pang, IOK-Hou
APPLICANT: Pang, IOK-Hou
APPLICANT: Clark, Abbot F.
TITLE OF INVENTION: Agents which regulate, inhibit, or modulate the activity and/or
TITLE OF INVENTION: expression of connective tissue growth factor (CTGF) as a uniqu
TITLE OF INVENTION: lower intraoscular pressure and treat glaucomatous retinopathies
TITLE OF INVENTION: neuropathies
TILE REFERENCE: 2354 WO F
CURRENT APPLICATION NUMBER: PCT/USO3/12521
CURRENT FILING DATE: 2003-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ellies, Debra
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATING BONE DEPOSITION
FILE REFERENCE: 40716-IP-017
                                                                             SOFTWARE: PatentIn version 3.1
                                                                                              NUMBER OF SEQ ID NOS: 2
                                                                                                                  PRIOR APPLICATION NUMBER: 60/376606 PRIOR FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 140 SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/388,970 PRIOR FILING DATE: 2002-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/464,368 CURRENT FILING DATE: 2003-06-16
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Alcon,
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 SRDEKE 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169 QKRAEE 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 GESFQSSCKYQ------CTCLDGSVGC-VPLCSVDVRLPSPDCPFPRRVKLPGKCCEEWV 165
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Shepard, Allan
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PCT-US02-18638A-46
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Search completed: July 24, 2003, Job time: 3.18936 secs
                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens PCT-US02-18638A-46
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                                                                                                                                                                                                                                                Query Match
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/298,159
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR FILING DATE: 2001-06-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: PCT/US02/18638A CURRENT FILING DATE: 2002-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PRETITLE OF INVENTION: OF CERVICAL CANCER
                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ
                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: MRI-035PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Millennium Pharmaceuticals, Inc. et al.
                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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nes 23; Conserv
                                                                                                                                      103 CIFGGTVYRSGESFQSSCKYQ---
                                                                                                                                                                             112 CVDAG-----GESHANNTKWKKDACTICECKDGQVTCFVEAC-----PPATCAVP--VN 158
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                                                                    156 LPGKCCEEWVC 166
                                                                                                      159 IPGACCP--VC
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23; Conserv
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                                                                                                                                                                                                                                                                                                                                                                          for Windows Version 4.0
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                13:13:04
                                                                                                                                                                                                          Score 77; DB 1; Length 349;
Pred. No. 0.82;
7; Mismatches 19; Indels
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Pred. No. 0.82;
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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    451899 segs, 118759770 residues
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/cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US08
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                US-10-9-884-319-2
US-10-153-57A-6
US-10-152-724A-4
US-09-373-967-2
US-09-887-527-60
US-10-028-072-142
US-10-121-049-142
US-10-133-904-142
US-10-175-746-142
US-10-176-918-142
US-10-176-918-142
US-10-176-918-142
US-10-176-918-142
US-10-176-918-142
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                                                                                                                                                                                                                                                                                SUMMARIES
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1753.524 Million cell updates/sec
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4, Appli
60, Appl
142, App
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-10-131-813A-14	-10-128-693A-14	0-127-901A-14	-10-127-839A-1	0-127-835A-14	-10-127-829A-14	-10-127-825A-14	0-124-824-14	-10-160-498-14	-10 - 140	-10-124-822-14	-10-124-819-14	-10-123-903-14	-10-123-292-14	-10-121-045-14	-10-140-928-14	-10-140-921-14	-10-123-261-14	-10-123-236-14	-10-123-108-14	0-143-032-14	-10-141-755-14	-10-121-050-14	-10-142-423-14	-10-123-262-14	-10-142-419-14	0-140-002-14	-10-143-114-14	-10-142-431-1	0-474-14
142,	142,	equence 142,	e 142,	142,	e 142,	142,	142,	142,	Sequence 142, App	142,	e 142,	142,	142,	e 142,	142,	-	142,	e 142,	e 142,	142,	142,	142,	142,	e 142,	e 142,	142,	142,	e 142,	2

ALIGNMENTS

US-09-840-707A-6

Sequence 6, Application US/09840707A Patent No. US20020077276A1 GENERAL INFORMATION:

RESULT 1

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                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 176
TYPE: PRT
                                                                                 Query Match
Best Local Similarity
Matches 176; Conserv
                                                                                                                                                                                                                OTHER INFORMATION: IL-1 receptor intracellular ligand protein OTHER INFORMATION: comprising amino acid sequence PUBLICATION INFORMATION: 5,817,476
PATENT DOCUMENT NUMBER: 5,817,476
PATENT FILING DATE: 1995-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/562,979
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/198,210
PRIOR FILING DATE: 1999-04-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/840,707A CURRENT FILING DATE: 2001-04-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Fredeking, Terry M.
APPLICANT: Ignatyev, George M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING HEMORRHAGIC VIRUS
TITLE OF INVENTION: INFECTIONS AND OTHER DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 26
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                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                              PUBLICATION DATE: 1998-10-06
                    1 IPRVDLRVWQDCCEDCRTRGQFNAFSYHFRGRRSLEFSYQEDKFTKKTRPRKIPSVGRQG
IPRVDLRVWQDCCEDCRTRGQFNAFSYHFRGRRSLEFSYQEDKPTKKTRPRKIPSVGRQG
                                                                                    Conservative
                                                                                                   100.0%;
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                                                                                 Score 962; DB 9;
Pred. No. 1.2e-89;
; Mismatches 0;
                                                                                                                            Length 176;
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                                                                                                                                                                                                                        Best Local Similarity Matches 176; Conserv
                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (617) 876-
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NOVEL INTERLEUKIN-1 RECEPTOR
INTRACELLULAR LIGAND PROTEINS AND INHIBITORS OF LIGAND
                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 176 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lin, Lih-Ling
   121
                                  121 ANNTKWKKDACTICECKDGQVTCFVEACPPATCAVPVNIPGACCPVCLQKRAEEKP 176
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                                                                                                                                                IPRVDLRVWQDCCEDCRTRGQFNAFSYHFRGRRSLEFSYQEDKPTKKTRPRKIPSVGRQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/083,516
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/487,942
FILING DATE: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANNTKWKKDACTICECKDGQVTCFVEACPPATCAVPVNIPGACCPVCLQKRAEEKP 176
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EHLSNSTSAFSTRSDASGTNDFREFVLEMQKTITDLRTQIKKLESRLSTTECVDAGGESH
                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/884,319 FILING DATE: 18-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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ZIP: 02140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    relephone:
                                                                                                                                                                                                                          Conservative
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(617) 876-5851
                                                                                                                                                                                                                                         100.0%;
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Pred. No. 1.2e-89;
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RESULT 4
US-10-152-724A-4
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Best Local S
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LENGTH: 176
TYPE: PRT
ORGANISM: Homo sapiens
                        SOFTWARE: PatentIn version 3.1 SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/10152724A Publication No. US20030082714A1
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                                                                     APPLICANT: HOLMES, Gregory
APPLICANT: KOLLE, Gabritel
APPLICANT: YAMADA, Toshiya
APPLICANT: YAMADA, Toshiya
APPLICANT: GEORGAS, Kylle
APPLICANT: GEORGAS, Kylle
TITLE OF INVENTION: NO. US20030082714A1el Nucleic Acid and Polypepti
FILE REFERENCE: P22378
CURRENT APPLICATION NUMBER: US/10/152,724A
CURRENT FILING DATE: 2002-05-23
PRIOR APPLICATION NUMBER: Australian App No. US20030082714A1PQ 4348
PRIOR FILING DATE: 1999-11-26
NUMBER OF SEQ ID NOS: 24
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APPLICANT: Ignatyev, George M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING HEMORRHAGIC VIRUS
TITLE OF INVENTION: INFECTIONS AND OTHER DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PUBLICATION INFORMATION:
PATENT DOCUMENT NUMBER: 5,817,476
PATENT FILING DATE: 1995-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/840,707
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: 09/562,979
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
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                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: LITTLE, Melissa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/038,557A CURRENT FILING DATE: 2002-06-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: IL-1 receptor intracellular ligand protein OTHER INFORMATION: comprising amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PUBLICATION DATE: 1998-10-06
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LENGTH: 1048
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nes 176; Conserv
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US-09-373-967-4
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US-09~373-967-2
; ORGANISM: Homo sapiens US-09-373-967-4
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APPLICANT: MCCOy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: DiBlasio-Smith, Elizabeth
                                                                                SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09373967 Publication No. US20020197666A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                              APPLICANT: DiBlasio-Smith, Elizabeth
APPLICANT: Widom, Angela
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: HUMAN CHORDIN-RELATED PROTEINS AND POLYNUCLEOTIDES ENCODING
FILE REFERENCE: GI 60/3A.DJ167DM665
                                                                                                                                                                                                                                                                                                                                 APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/373,967
CURRENT FILING DATE: 199-08-13
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
                                                                                                      SOFTWARE: PatentIn Ver. 2.0
                                                                                                                          CURRENT FILING DATE: 1999-08-13 NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/373,967
                                                                                                                                                                                                                                                                                          APPLICANT: Merberg, David APPLICANT: Treacy, Maurice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: HUMAN CHORDIN-RELATED PROTEINS AND POLYNUCLEOTIDES ENCODING
FILE REFERENCE: GI 6073A.DJ167DM665
FILE REFERENCE: GI 6073A.DJ167DM665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                               ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 16.6%; Score 160; DB 10; Local Similarity 43.1%; Pred. No. 5.3e-08;
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Similarity 45.1%; Pred. No. 9e-08;
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RESULT 8
US-10-028-072-142
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Best Local Similarity
Matches 22; Conserv
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APPLICANT:
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APPLICANT: HABERRY, MARTIN
APPLICANT: THIERAUCH, KARL-HEINZ
APPLICANT: THIERAUCH, KARL-HEINZ
TITLE OF INVENTION: COMBINATIONS AND COMPOSITIONS WHICH INTERFERE WITH
TITLE OF INVENTION: VEGF/VEGF AND ANGIOPOIETIN/TIE RECEPTOR FUNCTION
TITLE OF INVENTION: AND THEIR USE
FILE REFERENCE: SCH-1815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/887,527
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: DE 00250194.8
PRIOR FILING DATE: 2000-06-23
CURRENT APPLICATION NUMBER: US/10/028,072 CURRENT FILING DATE: 2001-12-19 PRIOR APPLICATION NUMBER: 60/049911 PRIOR FILING DATE: 1997-06-18
                                                                                     FILE REFERENCE:
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                                                                                                      TITLE OF INVENTION:
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
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                                                                                                                                                Watanabe, Colin K
Wood, William
                                                                                                                                                                                                                                                                                           Gerritsen, Mary E. Goddard, Audrey Godowski, Paul J.
                                                                                                                              Zhang
                                                                                                                                                                                         Stewart, Timothy A Tumas, Daniel
                                                                                                                                                                                                                                   Smith, Victoria
                                                                                                                                                                                                                                                    Gurney, Austin L. Sherwood, Steven
                                                                                                                                                                                                                                                                                                                                                           Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                 Filvaroff, Ellen
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                                                                                                                                                                                                                                                                                                                                                                                                                        DeForge, Laura
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43.1%; Pred. No. 1.8e-07;
ative 11; Mismatches 18;
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APPLICATION N
FILING DATE:
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NUMBER: 60/ : 1997-09-17 NUMBER: 60/ : 1997-08-26

60/056974 60/059113

APPLICATION NUMBER: 60/059115 FILING DATE: 1997-09-17

DR APPLICATION NUMBER: 60/059117
DR FILING DATE: 1997-09-17
DR APPLICATION NUMBER: 60/059122
DR FILING DATE: 1997-09-17
DR APPLICATION NUMBER: 60/059184
DR FILING DATE: 1997-09-17
DR APPLICATION NUMBER: 60/059263
DR FILING DATE: 1997-09-18
DR APPLICATION NUMBER: 60/059263
DR FILING DATE: 1997-09-18

APPLICATION NUMBER: 60/059352 FILING DATE: 1997-09-19 APPLICATION NUMBER: 60/059588 FILING DATE: 1997-09-19

APPLICATION NUMBER: 60/059836 FILING DATE: 1997-09-24

APPLICATION NUMBER: 60/062250 FILING DATE: 1997-10-17 APPLICATION NUMBER: 60/062285 FILING DATE: 1997-10-17

APPLICATION NUMBER: 60/062287 FILING DATE: 1997-10-17

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NUMBER: 60/081 1998-04-19 1998-04-15 1998-04-15 1998-04-15 1998-04-15 1998-04-15 1998-04-28 NUMBER: 60/081 1998-04-28 NUMBER: 60/083 1998-05-07 NUMBER: 60/084 1998-05-17 NUMBER: 60/085 1998-05-13 NUMBER: 60/085 1998-05-15 1998-05-15 NUMBER: 60/085 1998-05-16 NUMBER: 60/085 1998-05-16 NUMBER: 60/085 1998-05-20 NUMBER: 60/085 1998-05-26 NUMBER: 60/085 1998-05-26 NUMBER: 60/086 1998-05-26 NUMBER: 60/086 1998-05-26 NUMBER: 60/086 1998-06-04 NUMBER: 60/088	NUMBER: 60 1997-12-1 NUMBER: 60 1997-12-1 NUMBER: 60 1998-01-2 NUMBER: 60 1998-02-0 NUMBER: 60 NUMBER: 60 1998-03-1 NUMBER: 60

OR APPLICATION NUMBER: 60/063045
OR APPLICATION NUMBER: 60/063045
OR APPLICATION NUMBER: 60/063082
OR FILING DATE: 1997-10-24
OR APPLICATION NUMBER: 60/063127
OR FILING DATE: 1997-10-24
OR APPLICATION NUMBER: 60/063327
OR FILING DATE: 1997-10-27
OR FILING DATE: 1997-10-27
OR FILING DATE: 1997-10-27
OR APPLICATION NUMBER: 60/063329
OR FILING DATE: 1997-10-28
OR APPLICATION NUMBER: 60/063561
OR APPLICATION NUMBER: 60/063561
OR FILING DATE: 1997-10-28
OR APPLICATION NUMBER: 60/063704
OR FILING DATE: 1997-10-29
OR APPLICATION NUMBER: 60/063704
OR FILING DATE: 1997-10-29
OR APPLICATION NUMBER: 60/063703
OR APPLICATION NUMBER: 60/063733
OR FILING DATE: 1997-10-29
OR APPLICATION NUMBER: 60/063735

APPLICATION NUMBER: 60/062816 FILING DATE: 1997-10-24 APPLICATION NUMBER: 60/062814 FILING DATE: 1997-10-24

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OR APPLICATION NUMBER: 60/066364
OR FILING DATE: 1997-11-21
OR APPLICATION NUMBER: 60/066453
OR APPLICATION NUMBER: 60/066511
OR APPLICATION NUMBER: 60/066511
OR FILING DATE: 1997-11-24
OR APPLICATION NUMBER: 60/066770
OR FILING DATE: 1997-11-24
OR APPLICATION NUMBER: 60/069212
OR APPLICATION NUMBER: 60/069212
OR APPLICATION NUMBER: 60/069278

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OR APPLICATION NUMBER: 60/063738
OR FILING DATE: 1997-10-29
OR APPLICATION NUMBER: 60/063755
OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/064248
OR FILING DATE: 1997-11-03
OR APPLICATION NUMBER: 60/064809
OR FILING DATE: 1997-11-07
OR APPLICATION NUMBER: 60/065186
OR FILING DATE: 1997-11-12
OR APPLICATION NUMBER: 60/065846
OR FILING DATE: 1997-11-17
OR APPLICATION NUMBER: 60/065846
OR FILING DATE: 1997-11-17

FILING DATE: APPLICATION NUMBER: APPLICATION NUMBER: 60/ FILING DATE: 19/98-06-1

1998-06-17

60/089532 60/088858

APPLICATION NUMBER: 60/088810 FILING DATE: 1998-06-10

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RESULT 9
US-10-121-049-142
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; ORGANISM: Homo Sapien 
US-10-121-049-142
                                                               Prior Application removed - NUMBER OF SEQ ID NOS: 550 SEQ ID NO 142
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Best Local 9
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                                                                                                                  CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                    TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Baker, Kevin P.
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                                  TYPE: PRT
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mes 22; Conserv
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APPLICATION NUMBER: 60/091982
FILING DATE: 1998-07-07
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FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/090349
FILING DATE: 1998-06-23
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APPLICATION NUMBER: 60/091519
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                                                                                                                                                                                                           Zhang, Zemin
                                                                                                                                                                                                                       Wood, William
                                                                                                                                                                                                                                                                                                                             Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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                                                                                                                                                                                                                                                                            Stewart, Timothy A.
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                                                                                                                                                                                                                                                                                            Smith, Victoria
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Pred. No. 1.8e-07;
L1; Mismatches 18;
                                                                                                 See File Wrapper or Palm
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US-10-140-470-142
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US-10-123-904-142
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Best Local S
Matches 22
                                                                                                                                                                                                                               Sequence 142, Application US/10140470 Publication.No. US20030022331A1 GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 142
LENGTH: 1036
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APPLICANT:
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                                          Smith, Victoria
                                                       Sherwood, Steven
                                                                       Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
                                                                                                                       Gao, Wei-Qiang
Gerritsen, Mary E.
                                                                                                                                                    Desnoyers, Luc
Filvaroff, Ellen
                                                                                                                                                                                     DeForge, Laura
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Watanabe,Colin K
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Filvaroff, Ellen
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             Tumas, Daniel
                          Stewart, Timothy A.
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43.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                       Score 160; DB 15;
Pred. No. 1.8e-07;
1; Mismatches 18;
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Pred. No. 1.8e-07;
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US-10-176-918-142

; Sequence 142, Application US/10176918
; Publication No. US20030027275A1
; GENERAL INFORMATION:
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US-10-175-746-142
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Best Local Similarity
Watches 22; Conserve
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; ORGANISM: Homo Sapien
US-10-140-470-142
                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo Sapien US-10-175-746-142
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LENGTH: 1036
TYPE: PRT
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 142
LENGTH: 1036
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NUMBER OF SEQ ID NOS: 550
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CURRENT FILING DATE: 2002-06-19
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                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                      117 GESHANNTKWKKDACTICECKDGQVTCFVEACPPATCAVPVNIPGACCPVC 167
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Wood, William
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DeForge, Laura
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    See Palm or File Wrapper

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                                                                                                                                                                                                                               Score 160; DB 15;
Pred. No. 1.8e-07;
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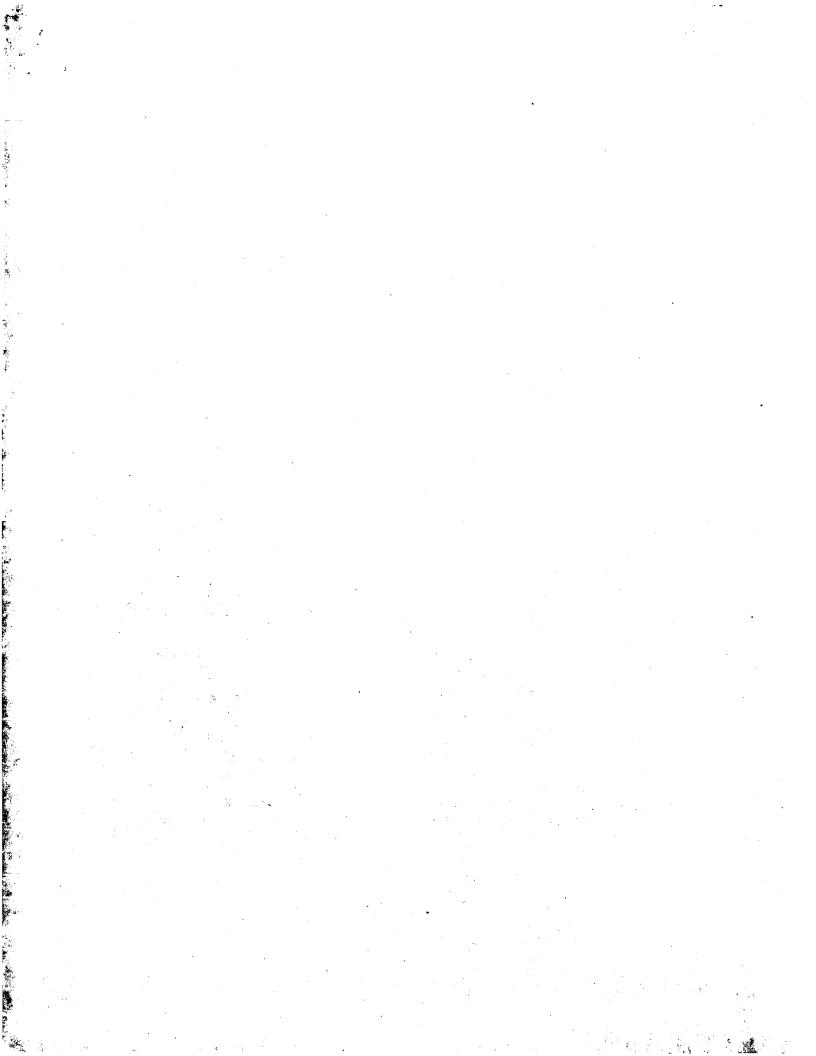
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Best Local Similarity
Watches 22; Conserva
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 142
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CURRENT FILING DATE: 2002-06-20
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                                                                                                   APPLICANT: Baker, Kevin P.
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C382
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TYPE: PRT
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              Gao, Wei-Qiang
                             Desnoyers, Luc
Filvaroff, Ellen
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Godowski, Paul J.
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                                                                DeForge, Laura
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US-10-176-921-142 ; ORGANISM: Homo Sapien US-10-176-921-142 SEQ ID NO 142 LENGTH: 1036 TYPE: PRT Sequence 142, *Publication No.* GENERAL INFORMATION: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C288
CURRENT APPLICATION NUMBER: US/10/176,921
CURRENT FILING DATE: 2002-06-20 APPLICANT: Prior Application removed NUMBER OF SEQ ID NOS: 550 APPLICANT: APPLICANT: APPLICANT: APPLICANT APPLICANT APPLICANT APPLICANT: APPLICANT: Zhang, Zemin Wood, William Tumas, Daniel Watanabe, Colin K Stewart, Timothy A Sherwood, Steven Goddard, Audrey Godowski, Paul J. Gurney, Austin L. Gerritsen, Mary E. Smith, Victoria See File Wrapper

or Palm

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RESULT 15
US-10-137-865-142
; Sequence 142, Apr
; Publication No. (
                                                                                                                                                                                                  Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550
SEQ ID NO 142
LENGTH: 1036
TYPE: PRT
ORGANISM: Homo Sapien
US-10-137-865-142
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Search completed: July 24, 2003, 13:14:50 Job time: 12.9198 secs
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                                                                                                                                                                                                                                                                                                                  APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P333071C154
CURRENT APPLICATION NUMBER: US/10/137,865
CURRENT FILING DATE: 2002-05-03
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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Sequence 99, Ap	Sequence 19, Appl	Sequence 7, Appl	Sequence 1, Appl	Sequence 37, Appl	•	Sequence 37, App		Sequence 37, App		Sequence 12, App	Sequence 12, App	Sequence 9, Appl	Sequence 9, Appl	-	-	-	Sequence 18, App

RESULT 1 US-08-726-525-2

ALIGNMENTS

; MOLECULE TYPE: protein US-08-726-525-2 Patent No. 578918 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION UMBER: 08/487,94 FILING DATE: 07-JUN-1995 ATTORNEY/AGENT INFORMATION: NAME: BIOWN, SCOtt A. REGISTRATION NUMBER: 32,724 REGISTRATION NUMBER: G152 TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 498-8224 TELEFAX: (617) INFORMATION FOR SEQ GENERAL INFORMATION: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compartible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICANT: Lin, Lih-Ling APPLICANT: Graham, James TITLE OF INVENTION: NOVEL INTERLEUKIN-1 RECEPTOR TITLE OF INVENTION: INTRACELLULAR LIGAND PROTEINS AND INHIBITORS TITLE OF INVENTION: BINDING SEQUENCE CHARACTERISTICS: CORRESPONDENCE ADDRESS: TYPE: amino acid STREET: 87 Camb: CITY: Cambridge TOPOLOGY: APPLICATION NUMBER: US/OFILING DATE: 07-OCT-1996 COUNTRY: LENGTH: ADDRESSEE: 02140 MA Application SE: LEGAL AFFAIRS, GENETICS INSTITUTE, INC 87 CambridgePark Drive 176 amino acids linear 876-5851 ID NO: 2: US/08726525 08/487,942 us/08/726,525 GI5258 OF LIGAND

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Query Match
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Matches 176; Conserv

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Score 962; DB 1 Pred. No. 8e-96; ; Mismatches

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NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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TITLE OF INVENTION: NOVEL INTERLEUKIN-1 RECEPTOR
TITLE OF INVENTION: INTRACELLULAR LIGAND PROTEINS
TITLE OF INVENTION: BINDING
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CORRESPONDENCE ADDRESS:
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COUNTRY:
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Pred. No. 8e-96;
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US-09-083-516-2
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Best Local :
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REFERENCE/DOCKET NUMBER:
REFERENCE/DOCKET NUMBER:
TELECHMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
TELEFAX: (617) 876-5851
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APPLICANT: Lin, Lih-Ling
APPLICANT: Graham, James
                                                                                                   APPLICANT: Lin, Lih-Ling
APPLICANT: Graham, James
TITLE OF INVENTION: NOVEL
TITLE OF INVENTION: INTRACT
TITLE OF INVENTION: BINDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                 NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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LENGTH: 176 amino acids
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NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
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APPLICATION NUMBER: US
FILING DATE:
CLASSIFICATION: 435
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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STREET: 6, Cambridge
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                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                             121 ANNTKWKKDACTICECKDGQVTCFVEACPPATCAVPVNIPGACCPVCLQKRAEEKP 176
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5. 5981482
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                               E: LEGAL AFFAIRS, GENE
87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: LEGAL AFFAIRS, GENETICS INSTITUTE, 87 CambridgePark Drive
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BINDING
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                                                                                                                                          NOVEL INTERLEUKIN-1 RECEPTOR
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                                                    GENETICS INSTITUTE,
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Pred. No. 8e-96;
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COMPUTER READABLE FORM:

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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/083,516
            CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                  SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 4
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                                                                                                                                                                 COUNTRY: USA
ZIP: 02110-2804
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                                                        APPLICATION NUMBER:
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APPLICATION NUMBER
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225 Franklin Street
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100.0%; Pred. No. 8e-96;
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INFORMATION FOR SEQ ID NO:
                                                                                                  TELEFAX: (415) 362-54
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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APPLICANT: Sasai, Yoshiki
TITLE OF INVENTION: Tissue Differentiation
TITLE OF INVENTION: Factor and Composition
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LENGTH: 940 amino acio
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                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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MOLECULE TYPE:
                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                         REGISTRATION NUMBER: 28,758
REFERENCE/DOCKET NUMBER: 3100.1
                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0 FILING DATE: 22-NOV-1994
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                             STRANDEDNESS:
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                                                                                                                                      TELEPHONE:
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                                                               ENGTH:
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amino acid
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                                                                                                                                                                                                               Siebert,
                                                                                                                                                                                                                                                                                                                                                                                                                                             CA
                                                               941 amino acids
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                             single
                                                                                                                                                                                                         J. Suzanne
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29.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tissue Differentiation Affecting
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Pred. No. 3.6e-07;
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US-08-820-170A-34; Sequence 34, Ap.
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                                   RESULT 8
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                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                        TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                             NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 401
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/31 FILING DATE: January 5, 1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
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                                                                                                                                                                                                                                                                                                           LENGTH:
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                                                                                      324 GRFFAENETWVVDSCTTCTCKKFKTICHQITCPPATCASPSFVEGECCPSCL 375
                                                                                                                      117 GESHANNTKWKKDACTICECKDGQVTCFVEACPPATCAVPVNIPGACCPVCL 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              737 SQPVHLPDQCCPVCEEKKEMREVKKP 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 AVPVNIPGACCPVCLQK---RAEEKP 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                639 KLNPR-----GEIRGQIHIPNSCES----GGVSLTPEEPEYEYEIYEEGRQRDPDDL 686
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                                                                                                                                                                         Similarity
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: New York
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   Application US/08820170A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08313288B
                                                                                                                                                                                                                                                                                                          1172 amino acids
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1185 Avenue of the Americas
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VENTION: CLONING, EXPRESSION AND USES OF A
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29.5%;
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                                                                                                                                                     Score 147; DB 1;
Pred. No. 4.8e-07;
3; Mismatches 24
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Pred. No. 3.6e-07;
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                                                                                                                                                         24;
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                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
                                                                                                                                                                                                                                                                                                                                     Patent No. 6005088
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                               APPLICANT:
          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEPAX: (202) 293-7860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion, Zinn, M
STREET: 2100 Pennsylvania Avenue,
                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                   APPLICANT:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                APPLICANT: TOYOMASA, KATAGIRI
TITLE OF INVENTION: HUMAN GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: TOYOMASA, ITTLE OF INVENTION:
                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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TELEFAX: 6491103
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                                                                                                             COUNTRY:
                                                                                                                               STATE: D.C.
                                                                                                                                                STREET: 2100 Pen
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/820,170A
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                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
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                                                                                                                                                                                                                                                                                                                                                     Application US/09055699
                                                                                                                                                                E: Sughrue, Mion,
2100 Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tsutomu, FUJIWARA
Takeshi, WATANABE
                                                                                                                                                                                                                                                                   Masato, HORIE
                                                                                                                 United States
                                                                                                                                                                                                                                                                                 Tsutomu, FUJIWARA
Takeshi, WATANABE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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30.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 137.5; DB 2
Pred. No. 3.1e-06;
                                                                                                                                                                   Zinn, Macpeak & Seas Avenue, N.W.
                                                                                                                                                                  Avenue,
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               Version #1.30
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APPLICATION NUMBER:

us/09/055,699

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                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens US-09-273-565-34
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                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn
SEQ ID NO 34
LENGTH: 810
                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 34, Appli
Patent No. 6166190
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TELEPAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 34:
                                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER APPLICATION NUMBER: 09/055,699
EARLIER FILING DATE: 1998-04-07
EARLIER APPLICATION NUMBER: 09/820,170
EARLIER FILING DATE: 1997-03-19
EARLIER APPLICATION NUMBER: JP 63410/1996
EARLIER FILING DATE: 1996-03-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: Q-53599
CURRENT APPLICATION NUMBER: US/09/273,565A
CURRENT FILING DATE: 1999-03-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: FUJIWARA, APPLICANT: WATANABE,
                                                                                                                                                                                                                                                                                                                                                                  EARLIER APPLICATION NUMBER: JP 69163/1997
EARLIER FILING DATE: 1997-03-05
NUMBER OF SEQ ID NOS: 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: HORIE, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 810 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 ACTICECKDGQVTCFVEACPPATC --- AVPVNIPGACCPVCLQK 170
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                                    130 ACTICECKDGQVTCFVEACPPATC---AVPVNIPGACCPVCLQK 170
                                                                            231 SDFLSLVQGIMDLQELLAKMTAKLNYAETRLSQLENCHCEKTCQVSGLLYRDQDSWVDGD 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32;
                                                                                                                       80 NDFREFV---LEMQKTITDLRTQIKKLESRLSTTE-----CVDAGGESHANNTKW-KKD 129
                                                                                                                                                                                 14.3%;
Similarity 30.8%;
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HCRNCTCKSGAVECRRMSCPPLNCSPDSLPVHIAGQCCKVCRPK 334
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                                                                                                                                                                                 Score 137.5; DB 3 Pred. No. 3.1e-06;
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Pred. No. 3.1e-06;
                                                                                                                                                                Mismatches
                                                                                                                                                                                                    DB 3;
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Best Local Similarity
Matches 32; Conserv
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NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn V
SEQ ID NO 34
LENGTH: 810
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Patent No. 63761
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SEQ ID NO 34
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CURRENT APPLICATION NUMBER: US/09/565,538
CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 09/273,565
PRIOR APPLICATION NUMBER: 09/273,565
                                                                                     PRIOR APPLICATION NUMBER: JP 6 PRIOR FILING DATE: 1996-03-19 PRIOR APPLICATION NUMBER: JP 6 PRIOR FILING DATE: 1997-03-05
                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/661,468 CURRENT FILING DATE: 2000-09-13 PRIOR APPLICATION NUMBER: 09/055,699 PRIOR FILING DATE: 1998-04-07
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                                                                                                                                                                        PRIOR APPLICATION NUMBER: 08/PRIOR FILING DATE: 1997-03-19
                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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PRIOR EILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: 08/820,170
PRIOR FILING DATE: 1997-03-19
                                                                                                                                                                                                                                                                                                              FILE REFERENCE:
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231 SDFLSLYQGIMDLQELLAKMTAKLNYAETRLSQLENCHCEKTCQVSGLLYRDQDSWVDGD
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                                            PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                          FUJIWARA, TSUTOMU WATANABE, TAKESHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/09661468
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                                                                                                                                                                                                08/820,170
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Pred. No. 3.1e-06;
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TING ENZYME
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RESULT 14
US-08-313-288B-20
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; ORGANISM: Homo sapiens
US-09-976-165-34
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                                                                                                                                                                                               Sequence 20, Applicat Patent No. 5750502 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 34
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Best Local :
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PRIOR FILING DATE: 1997-03-19
PRIOR APPLICATION NUMBER: JP 63410/1996
PRIOR FILING DATE: 1996-03-19
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CURRENT FILING DATE: 2001-10-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
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                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                    APPLICANT:
                                                                                                                             NUMBER OF SEQUENCES:
                        STATE: New York
                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity les 32; Conserv
                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1998-04-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
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                                                                                                                                                                                                                                                                                                                               291 HCRNCTCKSGAVECRRMSCPPLNCSPDSLPVHIAGQCCKVCRPK 334
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                                     New York
                                                                                                                                                                                                                                    Application US/08313288B
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                                                                     E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                             Jessell, Thomas M. and Avihu Klar
VENTION: CLONING, EXPRESSION AND USES OF A
                    USA
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                                                                                                                                              NOVEL SECRETED PROTEIN, F-SPONDIN
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Pred. No. 3.1e-06;
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US-08-749-169A-3
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TELEFAX: (6
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                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/749,169A
                                                  REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, Steven R.
REGISTRATION NUMBER: 32,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                 TELEPHONE:
                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                              STATE:
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                (617)
                                   (617) 498-8260
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876-5851 ID NO: 3

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; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-313-288B-20
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Rele
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: January 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40
TELECOMMUNICATION INFORMATION:
                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1170 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                         TITLE OF INVENTION: CHORDIN COMPOSITIONS NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                              CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  348 CKKVSCPIMPCSNATVPDGECCPRC 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 CFVEACPPATCAVPVNIPGACCPVC 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 REFVLEMQKTITDLRTQIKKLESRLSTTECVDAGGESHANNTKWKKDACTICECKDGQVT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RTIVTTLQDSIRKVTEENKELANELRRPPLCYHNGVQYRNNEEWTVDSCTECHCQNSVTI 347
                                                                                                                       Massachusetts
                                                                                                                                                           87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (212) 391-0526
                                                                                                       USA
                                                                                                                                                                                                                                                                                       Lavallie,
                                                                                                                                                                                                                                                                DeROBERTIS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                 Genetics Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
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                                                                                                                                                                                                                                                                                   Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/08/313, 288B
                                                                                                                                                                                                                                                                  Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 125; DB 1; Length 1170; Pred. No. 0.00011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                   Inc.
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-884-319A-2
962
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16:
17:
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1: /SIDS1/gcgdata/g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /SIDS1,
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1234.824 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length DB	Length		ID	Description
—	962	100.0	176	18	AAW19989	Type I, p80 IL-1-r
2	962	100.0	176	21	AAB37794	Human interleukin-
ω	962	100.0	550	22	AAE03865	Human gene 19 enco
4	962	100.0	550	23	ABG64535	Human albumin fusi
5	962	100.0	814	22	AAU23200	Novel human enzyme
6	962	100.0	1496	20	AAW81030	Melanoma associate
7	962	100.0	1496	21	AAY70469	Human p53 target m
8	962	100.0	1496	24	ABU03498	Angiogenesis-assoc
9	924.5	96.1	1498	22	ABB11587	Human percxidasin

WPI; 1997-052315/05 N-PSDB; AAT71216.

Interleukin-1 receptor intracellular ligand proteins and related DNA

ALIGNMENTS

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RESULT 1
AAW19989
Graham J, Lin L;
                                                                                07-JUN-1995;
                                                                                                  06-MAY-1996;
                                                                                                                    19-DEC-1996.
                                                                                                                                                                          IL; interleukin; receptor; ligand; screening assay; inhibitor; IL-1 mediated response; inflammation; inflammatory; antibody; intracellular domain; CANP; calcium activated neutral protease
                                                                                                                                                                                                               Type I, p80 IL-1-receptor intracellular domain ligand
                                                                                                                                                                                                                                27-AUG-1997 (first entry)
                                                                                                                                                                                                                                                                       AAW19989 standard; Protein; 176
                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                    AAW19989;
                                                            (GEMY ) GENETICS INST INC
                                                                                                                                       WO9640907-A1
                                                                                95US-0487942
                                                                                                  96WO-US06363.
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RESULT 2
AAB37794
    B
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                                                                                                                                                                                                          compounds
responses
colitis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW19989 represents a protein that has interleukin-1 receptor (IL-1-R) intracellular ligand activity. IL-1-R intracellular ligand proteins are used to screen for agents (e.g. antibodies) that are capable of inhibiting or blocking the binding of an IL-1-R intracellular ligand to the intracellular domain of IL-1-R, i.e. inhibitors of IL-1 activity. Such agents can be used to treat inflammatory conditions.
                                                                                                                                                                                                                                   Novel compositions comprising tetracycline or tetracycline-like compounds for the treatment and/or prevention of acute inflammaresponses and diseases, e.g. septic shock and immune complex-inc
                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-679646/66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fredeking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiinflammatory; haemostatic; antibacterial; immunosuppressive; immunomodulator; cardiant; cytostatic; neuroprotective; respirat inflammation; infection; sepsis; cachexia; autoimmune disorder; cardiovascular disorder; chronic myelogenous leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human interleukin-1 receptor intracellular ligand protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-FEB-2001
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compositions
                                                                                                                   Disclosure; Page 155-156; 183pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ANTI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Loca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTIBODY SYSTEMS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TM,
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                                     sequence is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9908-0301274.
methods containing tetracycline
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inflammatory bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English.
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Pred. No. 2e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA.
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relating to novel or tetracycline-like
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                                                                                                                                                                                                                                           complex-induced
                                                                                                                                                                                                                                                                                 inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             respiratory;
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RESULT 3
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Best Local S
Matches 176
                                                                                                                                                                                                                                                                                                                    angiogenic disorder; kidney disorder; gastrointestinal disorder; allergy; pregnancy-related disorder; endocrine disorder; infection; wound healing; cell culture; chemotaxis; vulnerary; binding partner identification; gene therapy; chromosome 2.
                                                                                                                                                                                                                                                                                                                                                                                 foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autolmmune disease; rheumatoid arthritis; Parkinson's disease; cognitive disorder; schizophrenia; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; inflammation; neurological disorder; Alzheimer's disease; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        multiple sclerosis, inflammatory responses associated with trauma, systemic inflammatory response syndrome (SIRS), adult respiratory distress syndrome (ARDS), acute liver failure, inflammatory bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        parasitic diseases, bacterial infections, sepsis, cachexia, autoimmune disorders, acute cardiovascular events, chronic myelogenous leukaemia a transplanted bone marrow-induced graft-versus-host disease, septic shoo immune complex-induced colitis, cerebrospinal fluid inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         compounds for treating and/or preventing acute inflammatory responses diseases. Such diseases include acute inflammatory conditions associat with viral haemornhagic diseases (including diseases caused by Bunyaviridea, Filoviridae, Flaviviridae or Arenaviridae viruses),
                               19-NOV-1999;
21-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE03865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                 15-NOV-2000; 2000WO-US31282
                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                     Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; secreted protein; proliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human gene 19
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Crohn's disease.
                                                                                                                                                                                                                                                                                                                  culture; therapy;
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176; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EHLSNSTSAFSTRSDASGTNDFREFVLEMQKTITDLRTQIKKLESRLSTTECVDAGGESH
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                               99US-0166414
2000US-0219665
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                                                                                                                                                                                                 /label=
2..550
                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
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                                                                                                                                                                               "Mature secreted protein"
                                                                                                                                                                                                                  signal_peptide
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Pred. No. 2e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein HOGCE48,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ
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RESULT 4
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ID ABG6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC 23 genes, based on the tissues in which they are most highly expressed, CC and include developing products for the diagnosis or treatment of CC proliferative disorders, cancer, tumours, foetal and developmental CC abnormalities, haematopoletic disorders, diseases of the immune system, CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, CC allergies, neurological disorders (e.g., Alzheimer's disease, CC Parkinson's disease), cognitive disorders, schizophrenia, asthma, CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, CC gastrointestinal disorders, pregnancy related disorders, endocrine CC disorders, and infections. The proteins can also be used to aid wound CC healing and epithelial cell proliferation, to prevent skin aging due to CC sunburn, to maintain organs before transplantation, for supporting cell CC culture of primary tissues, to regenerate tissues, to identify their CC cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties.

CC Antibodies specific for a protein of the invention can be used in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked CC immunosorbent assay (ELISA). The present sequence represents a human content of the invention of the presents and human contents of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                 Albumin fusion protein; therapeutic protein x; human albumin; human serum albumin; HSA; cancer; reproductive disorder; digestive disorder; immune disorder; endocrine disorder; haematopoietic disorder; neural disorder; connective disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amount of the new protein in a sample or by determining mutations in the new genes. Specific uses are described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or therapy. Pathological conditions can be diagnosed by determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD08283-AAD08355 represent cDNAs corresponding to 23 human protein genes, and AAE03818-AAE03870 represent the proteins take to a secreted protein fragments AAE03871-AAE03896 represent human secreted protein fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-343795/36.
N-PSDB; AAD08330.
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                                                                                                                       Human albumin
                                                                                                                                                               27-AUG-2002
                                                                                                                                                                                                         ABG64535
                                                                                                                                                                                                                                                ABG64535 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acid molecule encoding a human secreted protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                    ANNTKWKKDACTICECKDGQVTCFVEACPPATCAVPVNIPGACCPVCLQKRAEEKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPRVDLRVWQDCCEDCRTRGQFNAFSYHFRGRRSLEFSYQEDKPTKKTRPRKIPSVGRQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPRVDLRVWQDCCEDCRTRGQFNAFSYHFRGRRSLEFSYQEDKPTKKTRPRKIPSVGRQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                         fusion
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A
                                                                                                                                                                                                                                                Protein;
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                                                                                                                       protein #1210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention.
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for each of the
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s or variants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosting disorders such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes), haematopoietic disorders, neural disorders (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis, schizophrenia), and connective disorders (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-APR-2000;
25-APR-2000;
21-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;
neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
osteopathic; antiarthritic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to albumin fusion proteins conterapeutic protein X and human albumin (HA, also known as albumin, HSA). The proteins are useful for treating a disease of the content of the proteins are useful for treating a disease albumin, HSA).
                                                                                            AAU23200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New fusion protein for treating disease e.g. diabetes comprises albumin fused to a therapeutic protein {	extstyle -}
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                            Novel human enzyme polypeptide
                                                              18-DEC-2001
                                                                                                                            AAU23200 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fusion proteins of the invention.
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                                                                                                                                                                                                                                                                       435
                                                                                                                                                                                                                                                                                                                                      375
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                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                       EHLSNSTSAFSTRSDASGTNDFREFVLEMQKTITDLRTQIKKLESRLSTTECVDAGGESH 120
                                                                                                                                                                                                                                                                                                                                                   IPRVDLRVWQDCCEDCRTRGQFNAFSYHFRGRRSLEFSYQEDKPTKKTRPRKIPSVGRQG
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                                                                                                                                                                                                        ANNTKWKKDACTICECKDGQVTCFVEACPPATCAVPVNIPGACCPVCLQKRAEEKP
                                                                                                                                                                                                                                                                       EHLSNSTSAFSTRSDASGTNDFREFVLEMQKTITDLRTQIKKLESRLSTTECVDAGGESH
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2000US-199384P.
2000US-256931P.
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                                                             (first entry)
                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                   0;
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                               #286
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                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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as human serum
isease or
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494

Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;

ligase; hyperp autoimmune dis inflammatory dis blood-related blood-related nephrotropic; homo sapiens. W0200155301-A2 02-AUG-2001; 2 31-JAN-2000; 2 04-FEB-2000; 2 24-FEB-2000; 2 17-MAR-2000; 2 17-MAR
roliferal order; na disorder; na nticag 00000S-011 0000US-011 0000
neurological disorder; metabolic disorder, neurological disorder; metabolic disorder; metabolic disorder; cardiovascular disorder; reproductive disorder; infectious disorder; cytostatic; anti disorder; anti disord
der; e disorder; ti arthritic;
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14 - SEP - 2000 25 - SEP - 2000 27 - SEP - 2000 29 - SEP - 2000 20 - OCT - 200
2000US-023423 2000US-0234293 2000US-0234997 2000US-0235834 2000US-0235834 2000US-0235834 2000US-0235834 2000US-0236363 2000US-0236367 2000US-0236367 2000US-0236367 2000US-0236367 2000US-0236367 2000US-0237038 2000US-0237039 2000US-0241785 2000US-0241786 2000US-0241786 2000US-0241808 2000US-0241808 2000US-0241808 2000US-0244617 2000US-0246478 2000US-0246478 2000US-0246478 2000US-0246478 2000US-0246478 2000US-0246478 2000US-0246478 2000US-0246478 2000US-0246478 2000US-0246478 2000US-0246478 2000US-024678 2000US-024678 2000US-024678 2000US-024678 2000US-024678 2000US-0249210 2000US-0250391 2000US-0251988 2000US-0251866 2000US-0251866

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AAW81030
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CH MG5(
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                                                                                                                                                                                                                                                  RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to the isolation of novel human enzyme colored polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences canciding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lysses, isomerases or ligases. The sequences of the invention are useful in the citagenesis, treatment, prevention and/or prognosis of a wide range of citagenesis, treatment, prevention and/or prognosis of a wide range of citagenesis, including hyperproliferative disorders (e.g. cancer).

CC (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease), cetabolic disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), contabolic disorders (e.g. henylketonuria), inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. haemophilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. Influenza). The polynucleotides of the invention can also be used in gene therapy.

AND 22915-AAU 23814 represent the novel human enzyme polypeptides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Sim
Matches 176;
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08-DEC-2000;
11-DEC-2000;
                                                   MG50; melanoma gene-50;
T cell epitope; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JAN-2001;
                                  therapy;
                                                                                                        Melanoma associated
                                                                                                                                                                              AAW81030;
                                                                                                                                                                                                               AAW81030 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        specification,
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                                                                                                                                           10-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence data for this patent did not form part of the printed fication, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                   ANNTKWKKDACTICECKDGQVTCFVEACPPATCAVPVNIPGACCPVCLQKRAEEKP 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      814 AA;
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2000US-0251990.
2000US-0254097.
2000US-0259678.
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                                                                                                        antigen
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                                                   melanoma associated antigen; human;
lung cancer; rhabdomyosarcoma; diag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .0%; Score 962; DB 22; .0%; Pred. No. 1.4e-84;
                                                                                                        MG50
                                                                                                                                                                                                               1496
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                          melanoma, lung carcinoma and rhabdomyosarcoma cells, foetal brain, foetal heart and human placenta. The invention also provides T cell epitopes (see AAW81031-54) from MG50, including cytotoxic and helper T cell epitopes, antibodies that specifically bind to MG50 or an MG50 T cell epitope, recombinant vectors, and antigen presenting cells. Methods are provided for identifying an MG50 melanoma associated antigen in an individual and for identifying an immune response against an MG50 melanoma associated antigen, as well as methods of stimulating T lymphocytes that are reactive against cancer cells expressing MG50 and for treating an individual having cancer cells that express MG50. The products and methods can be used for the detection, treatment and prevention of NG50-expressing cancers, e.g. melanomas, lung cancer or
                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This polypeptide comprises a portion of a new human meassociated antigen, designated MG50. The amino acid so deduced from a cDNA clone (see AAV99922) isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell line MSM M-1 cDNA by subtrof MG50 cDNA was not obtained.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New MG50 melanoma associated antigen fragments - used to products for the detection, treatment and prevention of MG50-expressing cancers, e.g. melanoma, lung cancer or
                                                                                                  AAY70469
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                        1321
                                                                                                                                                                                                                               1381
                                                                                                                                                                         1441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    line MSM M-1 cDNA by subtractive hybridisation. The 5' 350\ \mathrm{cDNA} was not obtained. MG50 mRNA has been detected
                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                               176;
                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                     EHLSNSTSAFSTRSDASGTNDFREFVLEMQKTITDLRTQIKKLESRLSTTECVDAGGESH
                                                                                                  standard; Protein;
                                                                                                                                                                      ANNTKWKKDACTICECKDGQVTCFVEACPPATCAVPVNIPGACCPVCLQKRAEEKP
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                                                                                                                                                                                                                                                                                                                                                                                                      1496 AA;
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SOUTHERN CALIFORNIA.
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                                                                                                  1496
                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                                                                                                                        Score 962;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                melanoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5' region
                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                             Gaps
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Human p53 target molecule, 21-JUN-2000 (first entry)

PRG2 protein.

120 1380 60

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The present sequence is the protein encoded by PRG2 gene, that is C upregulated in response to induction of p53 activity in human colon CC cancer EBI cells. This sequence is the human homologue (hPxn) of CC cancer EBI cells. This sequence is the human homologue (hPxn) of CC prosophila peroxidasin gene dPxn, that is expressed in heart, placenta, CC spleen, ovary and intestines. PRG2 is involved in p53-mediated growth CC suppression pathways and plays a role in redox regulation. It is a cCC haem-peroxidase that increases the intracellular content of reactive convergen species (ROS). They are potential targets of p53 regulatory cCC cativity and are useful for modulation of cellular proliferation. PRG2 gene is localised to human chromosome 2p24.3. The PRG target molecules care cytostatic and immunomodulatory activity. PRG polynucleotides, proteins and antibodies are useful as diagnostic and therapeutic agents for detection and treatment of cancer and other proliferative diseases. The gene/cDNA may be used for gene threapy, to restore a gene function comparison of coll cycle arrest and/or as a modal of cancer auseaus as inducers of cell cycle arrest and/or as a modal of cancer auseaus be used to generate 'knockout' animals of the process can be used to generate 'knockout' animals.
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 71-74; 83pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                frame encoding human homolog of Drosophila melanogaster peroxidasin useful e.g. in detection and treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Horikoshi N,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New p53-inducible isolated nucleic acid molecule including open reading
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1441
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                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                             IPRVDLRVWQDCCEDCRTRGQFNAFSYHFRGRRSLEFSYQEDKPTKKTRPRKIPSVGRQG
                              ANNTKWKKDACTICECKDGQVTCFVEACPPATCAVPVNIPGACCPVCLQKRAEEKP 176
                                                                                                                            EHLSNSTSAFSTRSDASGTNDFREFVLEMQKTITDLRTQIKKLESRLSTTECVDAGGESH
                                                                                                                                                             EHLSNSTSAFSTRSDASGTNDFREFVLEMQKTITDLRTQIKKLESRLSTTECVDAGGESH 120
                                                                                                                                                                                                                                                        IPRVDLRVWQDCCEDCRTRGQFNAFSYHFRGRRSLEFSYQEDKPTKKTRPRKIPSVGRQG
ANNTKWKKDACTICECKDGQVTCFVEACPPATCAVPVNIPGACCPVCLQKRAEEKP 1496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1496 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of cancer susceptibility.
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shenk T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0098251.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 1..29
                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - Mature_human_PRG2_protein
"Homologue of Drosophila peroxidasin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 962; DB 21;
Pred. No. 3e-84;
                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1496;
                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                        0
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                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Qy Вb Š

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61

EHLSNSTSAFSTRSDASGTNDFREFVLEMQKTITDLRTQIKKLESRLSTTECVDAGGESH

120

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EHLSNSTSAFSTRSDASGTNDFREFVLEMQKTITDLRTQIKKLESRLSTTECVDAGGESH

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RESULT 8
ABU03498
ID ABU0
XX
AC ABU0
XX
                                                                                                                                                                                                                                                                     The present invention relates to methods and compositions for CC detecting an angiogenesis-associated transcript in a cell in a patient. The method involves contacting a biological sample from CC the patient with a polynucleotide that selectively hybridises to a sequence at least 80% identical to any of the angiogenesis-associated chuman polynucleotide sequences given in the specification. These CC angiogenesis-associated polynucleotide sequences comprise genes that CC exhibit changes in expression levels as a function of time in tissue undergoing angiogenesis. The method and the polynucleotide sequences of the invention are useful for diagnosing and treating angiogenesis of the invention are useful for diagnosing and treating angiogenesis associated diseases e.g. cancer. The polynucleotide sequences are also useful in the gene therapy of such disorders. The cangiogenesis-associated proteins encoded by the polynucleotide sequences are useful as a vaccine for therapeutic and prophylactic immunisation. ABU03456-ABU03569 represent angiogenesis-associated
                                                                                                     Matches 176;
                                                                                                                                                     Query Match
                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting angiogenesis-associated transcript in a cell for diagnosing and treating cancer by contacting a sample with a polynucleotide that exhibits changes in expression level as a function of time in tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                angiogenesis associated disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Angiogenesis-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABU03498;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   undergoing angiogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-FEB-2001;
19-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-FEB-2002;
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                                                                                                                                                                                                                                                          protein sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-NOV-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; angiogenesis-associated transcript; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EOSB-) EOS
                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2003-040681/03.
DB; ABX08782.
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                                                                                                                             Similarity
IPRVDLRVWQDCCEDCRTRGQFNAFSYHFRGRRSLEFSYQEDKPTKKTRPRKIPSVGRQG
                          IPRVDLRVWQDCCEDCRTRGQFNAFSYHFRGRRSLEFSYQEDKPTKKTRPRKIPSVGRQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 221-222; 291pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glynne R,
                                                                                                                                                                                                        1496 AA;
                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001US-0791390.
2001US-285475P.
2001US-310025P.
2001US-350666P.
2001US-334244P.
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                                                                                                                          100.0%;
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                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SR,
                                                                                                                        Score 962; DB 2
Pred. No. 3e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein sequence
                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aziz.
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                                                                                                                                                  DB 24;
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                                                                                                                                                     Length 1496;
                                                                                                     Indels
                                                                                                     0;
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1380
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Qγ

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RESULT 9
ABB11587
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   Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of identifying compounds which bind to polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell afferentiation activities; stem cell growth factor activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia;
                          thrombolytic activities; receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis. Depending on their biological activities, polypeptides and nucleon
                                                                                                                       haematopoiesis regulatory activity; tissue growth activity; immunomodulatory activity; activin- or inhibin-related activities; chemotactic or chemokinetic activities; haemostatic, thrombotic or chemokinetic activities;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human proteins and DNA encoding sequences useful for preventing treating or ameliorating a medical condition in a mammalian subtreating or ameliorating a medical condition in a mammalian subtreating or ameliorating a medical condition in a mammalian subtreating or ameliorating a medical condition in a mammalian subtreating or ameliorating a medical condition in a mammalian subtreating or ameliorating a medical condition in a mammalian subtreating or ameliorating a medical condition in a mammalian subtreating or ameliorating a medical condition in a mammalian subtreating or ameliorating a medical condition in a mammalian subtreating or ameliorating a medical condition in a mammalian subtreating or ameliorating a medical condition in a mammalian subtreating or ameliorating a medical condition in a mammalian subtreating or ameliorating a medical condition in a mammalian subtreating or ameliorating a medical condition in a mammalian subtreating or ameliorating a medical condition in a mammalian subtreating or ameliorating a medical condition in a mammalian subtreating or ameliorating a medical condition in a mammalian subtreating or ameliorating and a medical condition in a mammalian subtreating and a medical condition and a medi
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27-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB11587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC
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   invention are useful for preventing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arthritis
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)B; ABA08831.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oiesis regulation; tissue growth; chemotaxis; chemokinesis; thrombo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          osteopathic; vasotropic; cardiant; virucide; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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2000US-0560875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drmanac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NO:1957.
   or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mammalian subject
   ameliorating
                                 nucleotides
medical
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09-NOV-2000; 16-NOV-2000; 21-NOV-2000; 08-DEC-2000; 18-DEC-2000;

2000US-248642P. 2000US-249824P. 2000US-252824P. 2000US-254305P. 2000US-256448P.

08-NOV-2000;

08-NOV-2001; 16-MAY-2002

2001WO-US47420. 2000US-247505P

WO200238602-A2

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RESULT 10
AAO21660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with immunemodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders. Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a novel human
                                                                                                                                                                                                                                                                                                                                                            Antiarteriosclerotic; cytostatic; HIV; antiallergic; antianaemic; antiasthmatic; cardiant; vasotropic; neuroprotective; nootropic; SECP; anticonvulsant; antiparkinsonian; cerebrotective; antiinflammatory; immunosuppressive; human secreted protein; cell proliferative disorder; arteriosclerosis; cancer; autoimmune; inflammatory disorder; AIDS; allergy; anaemia; asthma; cardiovascular disease; developmental disorder; allergy; anaemia; asthma; cardiovascular disease; developmental disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g.,myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and
                                                                                                                                                                                                                                                                                                                     allergy; anaemia; asthma; cardiovascular disease; developmental disorder; ischaemic heart disease; congestive heart failure; neurological disorder; renal tubular acidosis; hypothyroidism; Alzheimer's disease; dementia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAO21660 standard; Protein; 1463
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                                                                                                                                                                                                                                                                                     Parkinson's disease; epilepsy; stroke; transgenic animal; gene therapy.
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97.2%;
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Pred. No. 1.
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RESULT 11
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorder e.g. arteriosclerosis, cancers; autoimmune/inflammatory disorder, AIDS, allergies, anaemia, asthma; cardiovascular disease e.g. congestive heart failure, ischaemia heart disease; developmental disorder e.g. renal tubular acidosis, hypothyroidism; neurological disorder e.g. Alzheimer's disease, dementia, Parkinson's disease, epilepsy or stroke. The SECP polynucleotide and polypeptide are further useful for analysing the proteome of a tissue or a cell type. The polynucleotide is useful for creating knockin humanised animals (pigs) or transgenic animals (mice or rats) to model human disease, and for somatic or germline gene therapy, and further for generating hybridisation probes useful in mapping the naturally occurring genomic sequence. This sequence represents a human secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated human secreted protein (SECP) polypeptide from 63 fully defined protein sequences given in the specification. The polypeptide is useful for the diagnosing/treating of disease with decreased/overexpression of SECP. Examples of disorders associated with abnormal expression of SECP include a cell proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ding L,
Lu DAM,
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                             WO200171042-A2
                                                          Drosophila melanogaster
                                                                                         pharmaceutical.
                                                                                                    Drosophila; developmental
                                                                                                                                  Drosophila melanogaster polypeptide SEQ
                                                                                                                                                                   26-MAR-2002
                                                                                                                                                                                               ABB57771;
                                                                                                                                                                                                                       ABB57771 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                              1342 DKIYVGEDARNVTVLAKTKF-----SQDFSTFAAEIQETITALREQINKLEARLRQAGCTD
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79; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                       Page 150-153;
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Thangavelu K,
                                                                                                                                                                                                                                                                                                                               AGGESHANNTKWKKDACTICECKDGQVTCFVEACPPATCAVPVNIPGACCPVC
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                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40.6%;
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                                                                                                      biology;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 390.5; Pred. No. 1e-2
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Elliott VS,
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                                                                                                      cell signalling;
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Lu Y, Gietzen KJ,
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J, Lal
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                                                                                                      insecticide
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Best Local
                                                                     antibody;
cataract;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  insecticides, therapeutics and pharmaceutical discloses genomic DNA sequences (ABL16176-ABL3 sequences (ABL01840-ABL16175) and the encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                CRIM-1; Chicken; human chromosome 2p21-16.3; ophthalmological; neuroprotective; renal; osteopathic; dental; vulnerary; immunoge antibody; gene therapy; neurodegenerative disease; eye disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ABB57737-ABB72072). The sequence data for this patent did not form part of the specification, but was obtained in electronic format direct
                           Gallus gallus
                                                                                                                                            Chicken CRIM1 protein.
                                                                                                                                                                                                      AAU07143;
                                                                                                                                                                                                                                 AAU07143 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genes from Drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAR-2000;
11-JUL-2000;
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                                                      abnormality;
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                                                                                                                                                                                                                                                                                                        PPGVDPLTPPEACCPHC
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                                                                                                                                                                                                                                                                                                                                                               VQLAAAPPQLVSKPKRSHCVDDKGTTRLNNEVWSPDVCTKCNCFHGQVNCLRERCGEVSC
                                                       bone morphogenic protein; promality; wound; $52.
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2000US-0614150
                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                 Protein; 1048
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25.9%;
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Pred. No. 8.3e-09;
7; Mismatches 71;
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                                                                     BMG;
                                                                       renal disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1527;
                                                                                                  immunogen;
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                                                                     abnormality;
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Location/Qualifiers

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Matches 23
                                                                                                                                invention or a mimetic which antagonises or mimics an activity of a CRIMI polypeptide may be used in a method for modulating the biological activity of a polypeptide of the bone morphogenic protein (BMP) family. In this way they may be used to prevent or treat an eye disease, especially cataract formation. They may also be used to treat neurodegenerative diseases, renal and kidney disease, bone and tooth abnormalities, wounds and skin damage, e.g. by use of the nucleic acid in gene therapy by using antibodies directed against CRIMI polypeptides. The present sequence represents chicken CRIMI (AKA S52).
                                                                                                                                                                                                                                                        and the encoded peptide (and mouse and chicken orthologues) that comprises a PGECCPLP group, an insulin-like growth factor binding protein (IGFBP)-like domain, cysteine-rich domain, e.g. CRIM1, interacts with and a transmembrane domain. The protein, e.g. CRIM1, interacts with peptides of the transforming growth factor superfamily. A composition comprising an expression construct comprising the nucleic acids of the
                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Fig 1; 169pp; English.
                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids from human chromosome 2p21-16.3 and the encoded peptide, useful for preventing, diagnosing and treating e.g. eye disease, especially cataract formation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                          invention relates to nucleic acids from human chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-343951/36.
 835
                        117 GESHANNTKWKKDACTICECKDGQVTCFVEACPPATCAVPVNIPGACCPVC 167
                                                    L Similarity
23; Conser
GKTYADEERWDIDSCTHCYCLQGQTLCSTVSCPPLPCAEPINVEGSCCPMC
                                                                                                         1048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000WO-AU01435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99AU-0004348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= CR_5
/note= "Cysteine
831..885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415..468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Cysteine rich repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           691..746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= CR_1
/note= "Cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    348..402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= CR_6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= CR_4
/note= "Cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= CR_3
/note= "Cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= CR_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=
                                                                 16.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Holmes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Conserved N-terminal motif"
                                                   11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6,
                                                   Score 163; DB 22;
Pred. No. 8.9e-07;
1; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Georgas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rich repeat'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ζ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kolle
                                                                             Length 1048;
                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wilkinson
                                                   0;
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                                                   Gaps
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                                                   0;
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RESULT 13
ABU70387
ID ABU70

ABU70387 standard; Protein; 293 AA

RESULT 14 AAY82775 ID AAY83

AAY82775 standard; Protein; 400 AA

밁 Ωy

91

Matches Query Match

l Similarity 22; Conser

Conservative

16.6%;

Score 160; DB 24; Pred. No. 3.4e-07; Mismatches

Length 293;

Indels

0;

Gaps

0;

117 GESHANNTKWKKDACTICECKDGQVTCFVEACPPATCAVPVNIPGACCPVC 167

GKAYADEERWDLDSCTHCYCLQGQTLCSTVSCPPLPCVEPINVEGSCCPMC

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CC polynoclectide encoding a polypeptide in the adipocyte cells, a CC recombinant host cell expressing at least one of the interacting compound in adipocyte cells, a SID (RTM)) polypeptide comprising a modulating compound in acid compensation of the sequences given in the specification (including its fragment or variant), a vector comprising the SID (RTM) polynucleotide comprising any of the 738 mucleotide sequences cc given in the specification (including its fragment or variant), a vector cc comprising the SID (RTM) polynucleotide, a recombinant host cell cc comprising the vector, a protein chip comprising the polypeptides and cc record comprising all or part of the data, listed in the specification. The complex, polypeptides, polynucleotides and compounds are useful for preventing or treating metabolic disorders such as obesity or diabetes. The polypucleotides are useful as probes or primers. The cc complex is particularly useful for identifying selected interacting cd domains (SID (RTM)) for screening drugs that modulate the protein content of the interaction, thus exhibiting the therapeutic effect. The present content content is sequence represents a SID (prey) protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                             by selecting a bait protein from a known adipocyte marker and then performing a yeast 2-hybrid selection to isolate prey proteins encoded members of an adipocyte cDNA library. The proteins are designated SID (RTM) (selected interacting domains) proteins. Also included are a polynocytide enroding a polynomerida in the adipocyte cDNA library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; prey; adipocyte; SID; selected interacting domain;
anorectic; antidiabetic; protein protein interaction; diabetes;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a complex between two interacting proteins addipocyte cells, given in the specification. The proteins are identi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 6; Page 114; 382pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        obesity or diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New complex between two interacting proteins in adipocyte cells, useful for identifying selected interacting domains that modulate protein interactions, or for preventing or treating metabolic disorders such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-103412/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-MAR-2001; 2001US-275734P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAR-2002; 2002WO-EP03768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200286122-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yeast 2-hybrid assay; metabolic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human adipocyte Selected Interacting domain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Legrain P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYBR-) HYBRIGENICS
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  293 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #18
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AAY82775

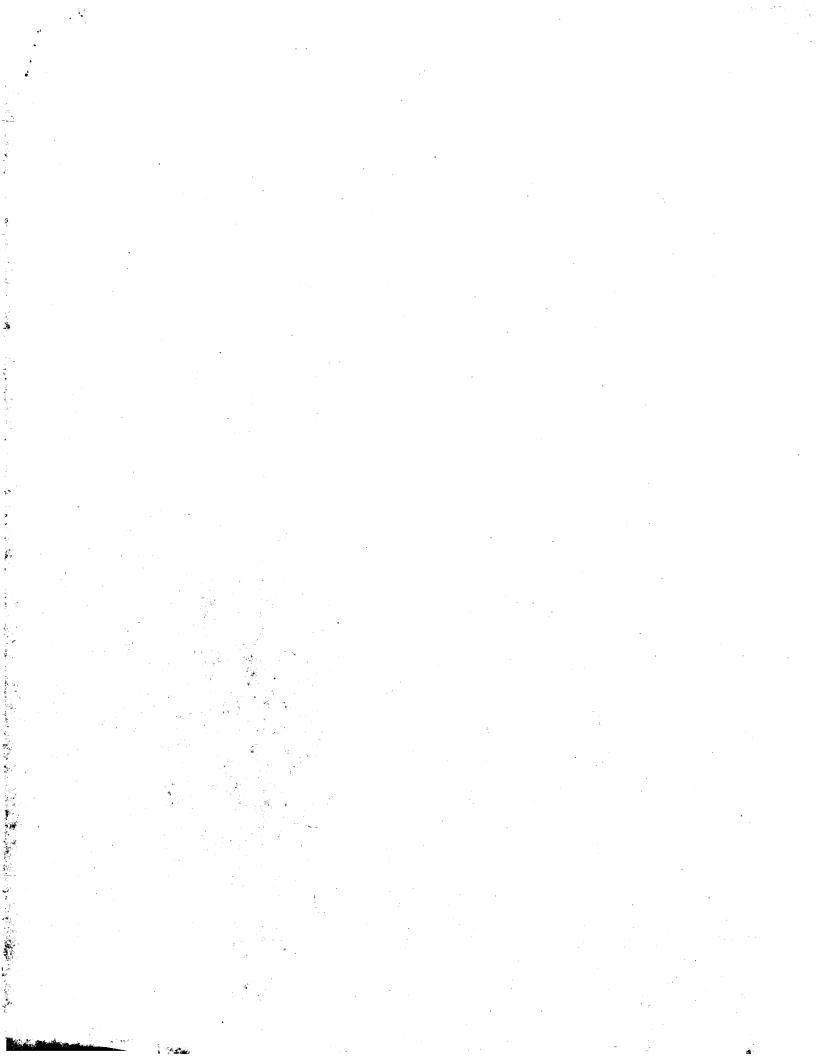
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useful in transplantation and treatment of conditions exhibiting a
clacrease in neuronal survival and repair. The proteins may also be
useful for the treatment of conditions related to other types of
tissue, such as nerve, epidermis, muscle, and other organs such as
liver, brain, lung, cardiac, pancreas, and kidney tissue. The
proteins may further be useful for the treatment of relatively
undifferentiated cell populations, such as embryonic cells, or stem
cells, to enhance growth and/or differentiation of the cells.
The proteins may also have other useful properties characteristic of
the TGF beta superfamily of proteins. Such properties include
angiogenic, chemotactic, and/or chemoattractant properties, and
effects on cells including induction or inhibition of collagen
synthesis, fibrosis, differentiation responses, cell proliferative
responses, and responses involving cell adhesion, migration, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The human chordin related protein and polynucleotides encoding them are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions which involve defects in cartilage, bone or connective tissue formation and damage to cartilage, bone or connective tissue, e.g. broken bones, congenital, trauma-induced, or oncologic-resection-induced craniofacial defects, periodontal disease, defects in the periodontal ligament or attachment apparatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 osteoporosis, burns, incisions or ulcers. The proteins may affect neuronal, astrocytic, and glial cell survival and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treating e.g. osteoporosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-AUG-1998;
06-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordin related protein; cartilage; bone; connective tissue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human chordin related protein (Clone dj167_2)
                                                                                                                                                                     extracellular matrices. These properties make the proteins potoagents for wound healing, reduction of fibrosis, and reduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     damage to the periodontal ligament or attachment apparatus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jacobs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             periodontal disease; o; astrocyte; glial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chemoattraction;
                                                                                                    scar tissue formation. Chordin-related proteins may also be useful for advancement of the onset of fertility in sexually immature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     periodontal disease; osteoporosis; burn; incision; ulcer; astrocyte; glial cell; transplantation; nerve; epidermis; inver; brain; lung; cardiac; pancreas; kidney; growth; liferentiation; TGF-Beta; angiogenesis; chemotaxis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polynucleotides encoding secreted human proteins, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000-205978/18.
DB; AAZ93171.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Z \
may also be useful in
                                                                    so as to increase the lifetime reproductive performance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 92-93; 105pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mccoy JM, Lavallie
Diblasio-smith E, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         broken bones, craniofacial burns, incisions or ulcers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0095880
99US-0306111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; collagen synthesis; fibrosis; cell adhesion; fertility; reproduction; haematopoiesis; tumour; dietary supplement; growth medium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e ER,
Widom
                                sheep and pigs. Chordin-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Collins-racie LA, A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         defects, peridontal disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Merberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuron;
                                                                                                                                                                                                             potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     also
inducing
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RESULT 15
AAY53033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                   07-MAY-1998;
02-JUN-1998;
22-JUL-1998;
                                                                                                                                                                                                                                                                                                                                              31-JUL-1998;
10-AUG-1998;
11-AUG-1998;
                    The present invention describes new human secreted proteins which were isolated from adult placenta, adult retina, foetal brain, foetal kidney, adult blood, adult brain, adult thyroid, adult bloader, adult nural tissue, adult testes, and adult lymph node cDNA libraries. The human secreted proteins, and the polynucleotides encoding them, are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. Suggested activities include nutritional activity, cytokine and activity and activities include nutritional activity.
                                                                                                                                                                                                                                                                 Jacobs K,
Merberg D,
                                                                                                                                            Claim 81; Page 423-424; 492pp; English.
                                                                                                                                                                        New polynucleotides encoding secreted human adult placenta, adult retina, fetal brain, f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     differentiation; immune stimulating; vaccine; suppression haematopoiesis regulation; tissue growth; activin; inhibir chemotactic; chemokinetic; haemostatic; thrombolytic; rece
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the differentiation of erythroid cells, for suppressing the development of gonadal tumors, or for augmenting the activity of BMPs. The proteins may also have value as a dietary supplement, as a component of cell culture media.
             and cell
                                                                                                                                                                                                                N-PSDB; AAZ33351
                                                                                                                                                                                                                            WPI; 2000-052937/04
                                                                                                                                                                                                                                                      DiBlasio-Smith E,
                                                                                                                                                                                                                                                                                                                                                                                                                                         07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9957132-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; secreted protein; nutritional; cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY53033 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY53033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ligand;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 GESHANNTKWKKDACTICECKDGQVTCFVEACPPATCAVPVNIPGACCPVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anti-inflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKAYADEERWDLDSCTHCYCLQGQTLCSTVSCPPLPCVEPINVEGSCCPMC
             proliferation/differentiation activity,
                                                                                                                                                                                                                                                                                мсСоу Лм,
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98US-0093712.
98US-0094935.
98US-0095880.
98US-0096068.
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Widom A;
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compus

Compugen Ltd

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Listing first 45 summaries
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sp_mhc:*
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sp_virus:*
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1 Q9CT39
1 Q8R2G6
3 Q8AXP2
1 Q8C043
    3 Q90X49
Q9JKW4
Q9D6Z4
Q8IVT6
Q8NBV1
Q8AXP3
Q8AXP3
Q9044R2
Q6068R7
Q8WW85
Q8WW85
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OBIVTO homo sapien
OBIDVI homo sapien
OBRAND gallus gall
OPH472 homo sapien
OBUMB57 homo sapien
OBUMB5 homo sapien
OBW486 mus musculu
OBR1054 mus musculu
                                                                                                                                                                                                             OBnhyB homo sapien
Q9ct39 mus musculu
OBr2g6 mus musculu
OBaxp2 gailus gall
OBaxp2 gailus gall
OBox49 brachydanio
O90x49 brachydanio
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ď	Q8lne4 oryza sativ	Q9zuk2 arabidopsis	Q8xil2 clostridium	Q				O59093 pyrococcus	. Q8gph9 staphylococ	\vdash		סי	٠.			Q8crz4 staphylococ	. Q9chn2 lactococcus	Q9fh23 arabidopsis	Q8ivc0 homo sapien	Q9kl63 vibrio chol	Q97kw9 clostridium	Q07427 carassius a	homo	Q96je3 homo sapien	Q96y62 sulfolobus	Q9r0m3 mus musculu	Q9r0m2 mus musculu	.Q8k1f8 mus musculu

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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Pukuda S.,
RA Alzawa K., Izawa M., Nishii K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishii K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Robert P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Frunno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Mayashinaki H., Toyo-oka K., Mang K.H., Weitz C., Whittaker C., Wilming L.,
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Mus musculus (Mouse).
Mus musculus (Mouse).
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Theria; Rodentia;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
261000TETRik protein (Fragment).
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Hayashizaki Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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EMBL; AK011256; BAB27498.1;
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76.2%;
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Pred. No. 2.9
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                          Equarin-L precursor.
Gallus gallus (Chicken).
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Q8AXP2; PRELIMINARY;
Q8AXP2;
01-MAR-2003 (TrEMBLrel. 2
01-MAR-2003 (TrEMBLrel. 2
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01-JUN-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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01-JUN-2002
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1; 62693C715C36F6AB CRC64;
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Metazoa;

Chordata;

Craniata;

Vertebrata;

Euteleostomi;

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Last Last

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SIGNAL
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Hong M., Ohta K., Kuriyama S., Tani
"Equarins: novel soluble molecules
chick embryonic lens.";
Submitted (JUN-2002) to the EMBL/Ge
EMBL; AB086824; BAC54279.1; -.
                                                                                                                                                                                                                                       Steroid sensitive gene-1
Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                    Q8C043;
01-MAR-2003 (TrEMBLrel.
                                                                                                    60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                          STRAIN=C57BL/6J; TISSUE=Olfactory brain; MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                         the RIKEN Genome Exploration Research Group Analysis of the mouse transcriptome based c
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                                                                                                                                                  FANTOM Consortium,
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ENCE 857 A
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  KKGGKTEQDGYQKPTNKHETQSPKKSVADLLGSFEGKRRLLLITAPKAENNMYVQQRDEY
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 Conservative
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                                                                                96621
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109322 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.4%;
                                              58.8%;
71.1%;
                                                                                                                                                                                                                                                   protein
                                                                                MW;
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                                                                                                                                                                                                                                                             Last
Last
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                                  Score 967.5;
Pred. No. 2.6e
7; Mismatches
                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1158.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred.
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1; 2E2DB2907899C2B5 CRC64;
                                                                                                                                                                                                                  Craniata; Vertebrata; Sciurognathi; Muridae;
D00D88D92159A9C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Galliformes;
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Mismatches
                                                                                                                                                                                                                                                   homolog.
                                                                                                                                                                                                                                                             sequence update) annotation update)
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                                                                                                                                                                                                                                                                                                                                                                   921
                                                                                                                                                                                                                                                                                                                                                                                        267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.3e-84;
                                              .6e-69;
                                                                                                                                                                                                                                                                                                           A
                                                         DВ
                                                                                                                          on
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d in the equ
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                                                                                                                                    Phase
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                                  11;
                                                        11;
                                                                                                                           functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  databases
                                                                               CRC64;
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                                   Indels
                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                  Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      equator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tanaka
                                                                                                                          annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               958;
                                   61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        region
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                                  Gaps
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Q9JKW4
ID Q9
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Best Local
                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-OCT-2002 (TrEMBLrel. 22, Last annotation update)
SC:BC2015.2 (Novel protein similar to rat steroid se
protein (SSG-1)).
SC:BE2015.2.
                                                                                                                                                                                                                                                                                                                                                                                      Submitted EMBL; AL59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q90X49
Q90X49;
01-DEC-2001
  Q9ЛКW4
                                                                                                                                                                                                                                                                                                                                                                           EMBL; AL590146; CASEQUENCE 867 AA;
                                                                                                                                                                                                                                                                                                                                                                                                           Lloyd
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii;
                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cyprinidae;
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                                                         806
                                                                                                    746
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                                                                                                                                               989
                                                                                                                                                                      175
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187; Conserv
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                                                                                                                                                                                                         ELRKEYGMTYNDFFMYLTDVDLRVKQYYEVPITMKSVFDLIDTFQSRIKDMEKQKKEGIV
                                                                                                                                                                                                                                                                                              KKGGK----TEQDGYQKPTNKHFTQSPKK-SVADLLGSFEGKRRLLLITAPKAENNMYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GMTYNDFFMVLTDVDLRVKQYYEVPITMKSVFDLIDTFQSRIKDMEKQKKEGIVCK----
                                                        WYPSPMWSMAIIYDLIDSMQLRRQEMAIQQSLGMRC
                                                                    WYPSPMWSMVIVYDLIDSMQLRRQEMAIQQSLGMRC
                                                                                                    VGTDLLDMGGVLELYPINGSATVEREGISATLYRDIRNYFQISPEYFSMLLVGKDGNVKS
                                                                                                                                              CKKEDKPRSLENFLSRFRWRRRLFVISAPNDEEWAYQQQLYALTSQACNLGLRHVSVLKL
                                                                                                                                                                       CKEE-----
                                                                                                                                                                                            ELRKEYGMTYNDFYVVLTDLDMKAKQYYEVPIAMKAVFDYIDTFSSRIREMEQQKRDGVT
                                                                                                                                                                                                                                       QQRDEYLEHVCEMAIRKVTIITIFGTFRNSTMKIDHYQLEKDKPMKGLRQEDLENQDLIM
                                                                                                                                                                                                                                                            QQRDEYLESFCKMATRKISVITIFGPVNNSTMKIDHFQLDNEKPMRVVDDEDLVDQRLIS
                                                                                                                                                                                                                                                                                  KKNGKKVPKILEKEDYQKPTKRPPPPPPPKGTLATFLDYFESRRRLILITSPTEENSMYI 565
                                                                                                                                                                                                                                                                                                                                                                          (OCT-2001) to the EMBL/GenBank/DDBJ databases 90146; CAC94894.1; -. 867 AA; 99920 MW; 3589AEBE33F41200 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGVLELFPINGSSIVEREDVPAHLVKDIRNYFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGVLELFPINGSSVVEREDVPAHLVKDIRNYFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QSLENFLSRFRWRRRLLVISAPNDEDWAYSQQLSALNGQACNFGLRHITILKLLGVGEEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LESFCKMATRRISVTIFGPVNNSSMKIDHFQLDNEKPMRVVDDDDLVDQHLISELRKEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LESFCKMATRKISVITIFGPVNNSTMKIDHFQLDNEKPMRVVDDEDLVDQRLISELRKEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KKAGKTEQDDNQKPTAKHLAPSPKKSVADLLGSFEGKRRLLLITTPKAENNMYVQQRDEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Danio.
                                                                                                                                                                                                                                                                                                                                Conservative
  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                             -VGGVLELFPINGSSVVEREDVPAHLVKDIRNYFQVSPEYFSMLLVGKDGNVKS
                                                                                                                                                                                                                                                                                                                                           58.1%;
55.7%;
                                                                                                                                                                                                                                                                                                                                40;
                                                                                                                                                                                                                                                                                                                              Score 956.5;
Pred. No. 2e-6
10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Teleostei; Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Danio rerio).
Craniata; Vertebrata;
  PRT;
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  385
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                                                                                                                                                                                                                                                                                                                               40;
                                                        841
                                                                             267
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Length

867; 69;

Gaps

231 745 178 685

Euteleostomi; Cypriniformes;

gene-1

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SEQUENCE FROM N.A.

2 STRAIN-C57BL/6J; TISSUE-Tonque;

2 STRAIN-C57BL/6J; TISSUE-Tonque;

3 Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

4 Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

4 A Arakawa T., Hara A., Fukunishi Y., Konno H., Kadachi J., Fukuda S.,

4 A Arakawa T., Hara A., Fukunishi Y., Konno H., Kasukawa T., Salto R.,

5 A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

6 A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto R.,

7 A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

8 A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

8 A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

8 A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

8 A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

8 A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

8 A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

8 A Kuehl R., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

8 A Kuehl R., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

8 A Kuehl R., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

8 A Kuehl R., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

8 A Kuehl R., Staubli F., Suzuki R., Tomita M., Wagner L.,

8 A Kuehl R., Staubli F., Suzuki R., Tomita M., Wagner L.,

9 A Kuehl R., Staubli F., Suzuki R., Tomita M., Wagner L.,

9 A Kuehl R., Staubli F., Suzuki R., Tomita M., Wagner L.,

9 A Kuehl R., Staubli F., Suzuki R., Tomita M.,

8 A Kuehl R., Staubli F., Suzuki R., Tomita M., Wagner L.,

9 A Kuehl R., Staubli F., Suzuki R., Tomita M.,

9 A Kuehl R., Staubli F., Suzuki R., Tomita M.,

9 A Kuehl R., Staubli F., Suzuki R., Tomita M.,

9 A Kuehl R., Staubli R., Tomita M.,

9 A Kuehl R., Staubli R., Tomita M.,

9 A Kuehl R., Staubli R., Tomita M.,

9 A Kuehl R., Kanda M., Kanda M., Kanda M., Kanda M.,

10 A Kuehl R., Kanda M., Kanda M., Kanda M.,

11 A Kuehl R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 158
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01-OCT-2000
01-OCT-2000
01-OCT-2002
Steroid sens
SSG-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
MEDLINE=21255622; PubMed=1
                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TremBLrel.
01-JUN-2001 (TremBLrel.
01-JUN-2001 (TremBLrel.
01-JUN-2001 (TremBLrel.
2610001E17Rik protein.
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01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning and characterization of a novel estrogen and is associated with mammary Endocrinology 142:2409-2418(2001).
EMBL; AF223677; AAF35351.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus
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158; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrembLrel. 15, Created)
(TrembLrel. 15, Last sequence up
(TrembLrel. 22, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=11356689;
halifour L.E., Alaoui-Jamali M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44066 MW;
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17,
17,
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Last
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Pred. No. 4.1e-56;
7; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                    Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46174E6FE7837346
                                                                                                                                                                                                                                                                                                                                                                                                                      sequence update) annotation update)
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gland
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thi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 that is regular carcinogenesis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
; Murinae; Mus
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                     nypotnetical protein FLJ90729
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia, Futheria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sasaki H.,
Suzuki H.,
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01-MAR-2003 (TrEMBLrel. 23, Last
01-MAR-2003 (TrEMBLrel. 23, Last
Similar to RIKEN cDNA 2610001E17
                                                          01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                      Submitted (DEC-2002) to t
EMBL; BC042105; AAH42105.
SEQUENCE 85 AA; 10174
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EMBL; AK009795; BAB26508.1; -.
MGD; MGI:1915146; 2610001E17R1k.
NCBI_TaxID=9606;
                    Mammalia; Eutheria; Primates;
                                                                                         Q8NBV1;
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Mammalia; Eutheria;
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Hayashizaki Y.;
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48; Conser
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Toyo-oka K., Wang K.H., Weitz C., Whittaker
ris A., Yoshida K., Hasegawa Y., Kawaji H.,
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                                                                                                    PRELIMINARY;
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Primates;
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Pred. No. 4.2e-13;
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                   Craniata; V
Catarrhini;
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AC Q8AXP4
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QC Eukaa
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01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hattori A., Okumura K., Iwayanagi T., Ninomiya K.; "NEDO human cDNA sequencing project."; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AK075210; BAC11475.1;
                                                                                                                                                                                                            SEQUENCE FROM N.A.
Hong M., Ohta K., Kuriyama S., Tanihara H., Ya
"Equarins: novel soluble molecules expressed i
chick embryonic lens.";
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                       Equarin-S precursor.
Gallus gallus (Chicken).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K., Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
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                                                                                             KGGKTEQDGYQKPTNKHFTQSPK-KSVADLLGSFEGKRRLLLITAPKAENNMY-----VQ
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            ---RLISELRKEYGMTYNDFFMVLTDVDLRVKQYYEVPITMKSVFDLIDTFQSRIKDMEK
                                    KNDVY----CELAERHIQQIVLFHEEGE------
                                                                               KSEMIKDEGISTASQSRAVRFPSGSSSPNVLASFAGKNRVWVISAPHASEGYYRLMMSLL
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67676 MW;
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29.3%;
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Last annotation updat
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                                                                                                                                      Pred. No.
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O60687

OFFICIAL PREMARY

OFFICE OFFI
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InterPro; IPR003410; Hyalin.
InterPro; IPR000436; Sushi_SCR_CCP.
Pfam; PF00494; HYR; 1
Pfam; PF00494; sushi; 3.
Pfam; PF00084; sushi; 3.
SMART; SM00032; CCP; 3.
SMART; SM00035; CCP; 3.
        SRPUL.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Eukaryota: Futheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wilson S.;
Submitted (OCT-2000) to the
EMBL; AL391688; CAC16060.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; V.
Mammalia; Eutheria; Primates; Catarrhini;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                   GRIREQQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVADLLGSFEGKRRLLLITAPKAENNMYVQQRDEYLESFCKMATRKISVITIFGPVNNST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RTTTLPTTTTATRATTRTVTTASRPTTTTTPLPTTQRTWTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DGNVKSWYPSPMWSMVIVYDLIDSMQLRRQEMAIQQSLGMRCQKMSMQAMVTI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QKKEGIV--CKEEVGGVLELFPINGSSVVEREDVPAHLVKDIRNYFQVSPEYFSMLLVGK
                                                                                                                                                                                                                                                                                                   VTPEEIFTFIDDYLLSNQELTQRREQRDICE
                                                                                                                                                                                                                                                                                                                                         ITMKSVFDLIDTFQSRIKDMEKQKKEGIVCK 176
                                                                                                                                                                                                                                                                                                                                                                                                                      MKIDHFQLDNEKPMRVVDDEDLVDQRLISELRKEYGMTYNDFFMVLTDVDLRVKQYYEVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAAGLLDQFYEKQRLLIISAPDPSNRYYKMQISMLQQSTCGLDLRHVTIIELVGQPPQEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIPKLMSFLKLEKG----KFGMVLLKKTLQVEERYPYPVRLEAMYEVID--QNPIRKIEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          410 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TTEMBLrel. 16, Created)
(TTEMBLrel. 16, Last sequence update)
(TTEMBLrel. 23, Last annotation update)
(Sushi-repeat-containing protein) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46781 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 147.5;
Pred. No. 0.0
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                    Craniata; V
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D32228E1AA1AF370 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                       Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                        410
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                    Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     410;
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Best Local S
Matches 40
                                                                                                                                     Query Match
Best Local
                                                                                                                  Matches
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01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                        Pfam; PF02494; HYR; 1.
Pfam; PF00084; sushi; 3.
SMART; SM00032; CCCF; 3.
PROSITE; PS00086; CYTOCHROME_P450; 1.
SEQUENCE 465 AA; 52957 MW; 3D7229487DA1B8BD CRC64;
                                                                                                                                                                                                                                                                                                                           Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases EMBL; BC020733; AAH20733.1; -. InterPro; IPR001128; Cytochrome_P450. InterPro; IPR000410; Hyalin. InterPro; IPR00046; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
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Pfam; PF00084; sushi; 3.
PROSITE; PS00086; CYTOCHROME_P450; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases EMBL; AF060567; AAC15765.1; - EMBL; AF393649; AAM73693.1; - InterPro; IPR001128; Cytochrome_P450.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003410; Hyalin.
InterPro; IPR000436; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Huang C.-H., Chen H., Peng J., Chen Y.;
"Cloning and characterization of the sushi-repeat containing p. (SRP) as a novel interaction partner of Rh type C glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQUENCE FROM N.A.
                   330
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                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAAGLLDQFYEKQRLLIISAPDPSNRYYKMQISMLQQSTCGLDLRHVTIIELVGQPPQEV
                                                                SVADLLGSFEGKRRLLLITAPKAENNMYVQQRDEYLESFCKMATRKISVITIFGPVNNST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    465 AA;
                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52971 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                             Score 147.5;
Pred. No. 0.00
29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4D752B187FF3EFB8 CRC64;
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                                                                                                ປ.0012;
67;
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                                                                                                                                                         DB 4;
                                                                                                                                                            Length
                                                                                                               Indels
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RESULT 15
Q8K4W6
Search completed: July 24, Job time: 42.5854 secs
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Best Local Similarity
                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF393647; AAM73690.1; JEMBL; AF393641; AAM73690.1; JEMBL; AF393642; AAM73690.1; JEMBL; AF393643; AAM73690.1; JEMBL; AF393644; AAM73690.1; JEMBL; AF393646; AAM73690.1; JEMBL; AF393646; AAM73690.1; JEMBL; AF393646; AAM73690.1; JEMBL; AF393646; AAM73690.1; J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UI-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Sushi-repeat containing protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                Pfam; PF02494; HYR; 1.
Pfam; PF00084; sushi; 3.
SMART; SM00032; CCP; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8K4W6;
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                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                    PROSITE; PS00086; CYTOCHROME_P450; 1.
NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Huang C.-H., Chen H.; Peng J., Chen Y.;
"Cloning and characterization of the sushi-repeat containing p (SRP) as a novel interaction partner of Rh type C glycoprotein (RhCG).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                          InterPro;
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                                                                                                                                 MKIDHFQLDNEKPMRVVDDEDLVDQRLISELRKEYGMTYNDFFMVLTDVDLRVKQYYEVP 145
                                                        VTPEEIFTFIDDYLLSNEELARRVEQRDLCE
                                                                                    ITMKSVFDLIDTFQSRIKDMEKQKKEGIVCK 176
                                                                                                                                                                        SAAGLLDQFYEKQRLLIVSAPDPSNRYYKMQISMLQQSTCGLDLRHVTIIELVGQPPQEV
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Title: Perfect score:

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Scoring table: Sequence

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  SYK_HAEIN
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Y602_METUA
RAS2_HYDMA
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POAST
IF2P_SULSO
NEST_HUMAN
IQG1_HUMAN
IQG1_HUMAN
RAS_LACBI
GATB_METUA
OPPF_MYCGE
DPOL_HSVII]
RA50_METUA
CC31_YEAST
RA50_SULAC
SLPH_BRECH
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T2RZ_HUMAN
T2RZ_HUMAN
T2RZ_FOYTHO
IF2P_SULAC
YC14_METUA
Y772_ARCFU
TTP1_YEAST
Y772_HUMAN
HEP2_HUMAN
PFID_BUCAP
SRC1_YEAST
IF2P_PYRAB
FIB_BOVIN
RNSZ_SOLTU
Y541_PYRHO
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Q58611
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SMART; SM00032; (
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MEDLINB-96184379; pubMed-8612783;
Pan J., Nakanishi K., Yutsudo M., Inoue H., Li Q., Oka K.,
Yoshioka N., Hakura A.;
"Isolation of a novel gene down-regulated by v-src.";
"APPLICATION OF AND POLYMAVIRUS TRANSFORMED PAPILLOMAVIRUS TYPE 16 E6E7 AND POLYMAVIRUS LARGE T. S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SRPX_RAT STANDARD; PRT; 464 AA. 063769; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Sushi repeat-containing protein SRPX precursor regulated by V-SRC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
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Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Rode
MCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                          InterPro; IPR003410; Hyalin.
InterPro; IPR000436; Sushi_S
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2; CCP; 3.
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SEQUENCE
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shamfen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratte P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SRPX_HUMAN STANDARD; PRT; 4
P78539; Q99652; Q99913;
O1-NOV-1997 (Rel. 35, Created)
O1-NOV-1997 (Rel. 35, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
Sushi repeat-containing protein SRPX p
                                                                                                                                                                                                                                                                                                                                          Dry K.L., Aldred M.A., Edgar A.J., Brown J., Manson F.D. Prosser J., Hardwick L.J., Lennon A.A., Thomson K., van Kurnit D.M., Bird A.C., Jay M., Monaco A.P., Wright A.F. "Identification of a novel gene, ETX1 from Xp21.1, a can for X-linked retintis pigmentosa (RP3).";
Hum. Mol. Genet. 4:2347-2353(1995).
                                                                                                                                                           MEDLINE=22388257;
                                                                                                                                                                                                                                                                                   MEDLINE=97306278; PubMed=9162095; Nangaku M., Shankland S.J., Kurokawa K.,
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
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                                                                                                                                                                                           SEQUENCE FROM
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                                                                                                                                                                                                                       [mmunogenetics
                                                                                                                                                                                                                                                    "Cloning
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renz B., Apfelstedt-Sylla E., Wittwer B., Ross N.
gene (SRPX) encoding a sushi-repeat-containing
pattents with x-linked retinitis pigmentosa.";
m. Mol. Genet. 4:2339-2346(1995).
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) sapiens (Human).

Metazoa; Chordata;
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                                                                                                                                                           PubMed=12477932;
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EMBL; S82496; AAB37379.1; --
EMBL; S82496; AAB37379.1; --
EMBL; U61374; AAB40715.1; --
EMBL; BC020684; AAH20684.1;
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Pfam; PF00084; sushi;
SMART; SM00032; CCP;
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SIGNAL
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ALTERNATIVE PRODUCTS:
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Comment=Additional isofor;
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IPR000436; Sushi_SCR_CCP
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A Whiting M., Madan A., Young A.C., Green E.D., Dickson M.C., A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., A Rodriguez A.C., Grimwood J., Schmutz J., Wars R.M., Stalska U., Smailus D.E. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; Young S.J.M., Marra M.A.; The Generation and initial analysis of more than 15,000 full-le "Generation and mouse cDNA sequences."; Thuman and mouse cDNA sequences."; RI human and mouse cDNA sequences."; RI Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). CC CC. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). CC CELL ADHESION TO CELLS OTHER THAN THE PIGMENT EPITHELIU
                                                                                    POSSIBLY SURFACE OF PHOTORECEPTOR CELL
                                                                                                                                                                                                                                                                                                                                                                                         A.C., Shevchenko
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modified and this statement is not removed. entities requires a license agreement (See TISSUE SPECIFICITY: RETINA AND HEART; LESS IN PLACENTA, PANCREAL LUNG, LIVER, SKELETAL MUSCLE, KIDNEY, AND BRAIN.

DOMAIN: THE SUSHI DOMAINS HAVE 6 CONSERVED CYSTEINES INSTEAD OF FOUR. A SIMILAR DOMAIN WITH ONLY 2 CONSERVED CYSTEINES IS LOCATED BETWEEN SUSHI DOMAINS 2 AND 3. SIMILARITY: Contains 3 Sushi (SCR) domains SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the ENEUropean Bioinformatics Institute. There are no rest -profit institutions as long Sequence=VSP_004430; as its content http://www Usage bу restrictions and EMBL a collaboration for LOCATED

SUSHI REPEAT-CONTAINING PROTEIN SRPX.
SUSHI 1.
SUSHI 2.
SUSHI-LIKE.
SUSHI-LIKE.
SUSHI-LIKE.
BY SIMILARITY.
BY SIMILARITY. /FTId=VAR_005625 S -> F. VSKRRCLIGESGH /FTId=VAR_005624 /FTId=VSP_004430 Sushi; Alternative (in isoform splicing;

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RESULT 3
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SEQUENCE
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Q9Y6Q2;
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16-OCT-2001
28-FEB-2003
                                                                                                                 Transcription regulation; Nuclear protein.
DOMAIN 44 150 PRO/SER/THR-RICH
                                                                                                                                                            Pfam; PF00928; Adap_com
Pfam; PF03153; TFIIA; 1
                                                                                                                                                                                                                                                                                EMBL; AF026169; AAD
HSSP; P32773; 1YTF.
                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Identification of a general transcription homolog selectively expressed in testis.", J. Biol. Chem. 274:18040-18048(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                 entities requires a
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                                                                                                                                                                                                        InterPro;
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    Mismatches
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factor (SALF)
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                                                                                                                                                                                                                                         activity;
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                                       DB 1;
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  84;
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  37;
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RESULT 4
IF2P_PYRHO
                                                                                                                                                                                                                                                                                                                     Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y
Yamamoto S., Sekine M., Baba S.-I., Kosuqi H., Hosoyama A.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohi
Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi
Masuchi Y., Shizuya H., Kikuchi H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    058822;
15-DEC-1998
                                                                                                                                               -i- FUNCTION: FUNCTION IN GENERAL TRANSLATION INITIATION BY PROMOTING THE BLYDING OF THE FORMYLMETHIONINE-TRNA TO RIBOSOMES. SEEMS TO FUNCTION ALONG MITH EIF-2 (BY SIMILARITY).
-i- PTM: THIS PROTEIN UNDERGOES A PROTEIN SELF SPLICING THAT INVOLVES
                                                                                                                                                                                                                                                 "Complete sequence and gene organization of the genome of a thermophilic archaebacterium, Pyrococcus horikoshli OT3."; DNA Res. 5:55-76(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable translation initiation factor IF-2 [Contains: Pho infB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pyrococcus horikoshii.
Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98344137; PubMed=9679194;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=53953;
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                    MISCELLANEOUS: THE INTEIN INTERRUPTS THE SIMILARITY: BELONGS TO THE IF-2 FAMILY. SIMILARITY: IN THE INTEIN SECTION; BELONG
ENDONUCLEASE FAMILY.
                                                                                             A POST-TRANSLATIONAL EXCISION OF THE INTERVENING FOLLOWED BY PEPTIDE LIGATION (POTENTIAL).
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                          BELONGS
                                                                        GTP BINDING
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                          THE
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                                                                                                                          REGION
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K.,
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InterPro; IPR004544; TIF_aIF-2
Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
PRINTS; PR00379; INTEIN.

InterPro;

IPR004042; Intein_endonuc. IPR005225; Small_GTP. IPR004544; TIF_aIF-2.

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RESULT 5
IF2P_SULA
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Best Local S
Matches 40
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SMART; SM00306; HintC; 1.

SMART; SM00306; HintN; 1.

TIGRPAMS; TIGR004491; aIF-2; 1.

TIGRPAMS; TIGR01443; intein_Cterm; 1.

TIGRPAMS; TIGR01445; intein_Nterm; 1.

TIGRPAMS; TIGR00231; small_GTP; 1.

PROSITE; PS01176; IP2; PALSE_NEG.

PROSITE; PS01816; INTEIN_C_TER; 1.

PROSITE; PS50819; INTEIN_C_TER; 1.

PROSITE; PS50819; INTEIN_N_TER; 1.
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15-DEC-1998
15-DEC-1998
28-FEB-2003
   use by modified
                         between
the Euro
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                                                  This
                                                                        Reeling P.J., Baldauf S.L., Doolittle W.F., Zillig W., Klenk H.-P.; "An inf8-homologue in Sulfolbus acidocaldarius.";

Syst. Appl. Microbiol 19:312-321(1996)
-i- FUNCTION: FUNCTION IN GENERAL TRANSLATION INITIATION BY PROMOTING THE BINDING OF THE FORMYLMETHIONINE-TRANA TO RIBOSOMES. SEEMS TO FUNCTION ALONG WITH EIF-2 (BY SIMILARITY).

-i- SIMILARITY: BELONGS TO THE IF-2 FAMILY.
                                                                                                                                                                                                 Sulfolobus
                                                                                                                                                                                                                      Sulfolobus acidocaldarius
                                                                                                                                                                                                                                                Probable
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                                                                                                                                                                                                                                                                                                                       SULAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                   NCBI_TaxID=2285;
                                                                                                                                                                                                           Archaea; Crenarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Endonuclease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Autocatalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Initiation factor; Protein biosynthesis; GTP-binding;
                        European Bioinformatics Institute.
                                   SWISS-PROT entry is copyright. It is produced through
en the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                          SULAC
                                                                                                                                                                                                                                                                                                                                                                                                                    827
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                non
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                                                                                                                                                                                                                                                                                                                                                                                                                                        PMRVVD-----DEDLVDQRLISELRKEYGMTYNDFFMVLTDVDLR-VKQYYEVPITMKS-
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578
1044
                                                                                                                                                                                                                                                         (Rel. 37,
(Rel. 37,
(Rel. 41,
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467
   -profit
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1044
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25.5%;
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Last annotation update)
initiation factor IF-2 (
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                                                                                                                                                                                                                                                                                  Created)
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                                                                                                                                                                                                           Thermoprotei;
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Pred. No.
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PROBABLE TRANSLATION INITIATION FACTOR IF-2, 1ST PART (POTENTIAL).

PHO INTE INTEIN (POTENTIAL).

PROBABLE TRANSLATION INITIATION FACTOR
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
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            as long
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RESULT 6
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YC14_METJA
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Best Local S
Matches 45
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InterPro; IPR005225; Small_GTP.
InterPro; IPR004544; TIF_aIF-2.
Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
PRINTS; PR00315; ELONGATNECT.
                                          STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE=96337999; PubMed=8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dugherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Eraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NP_BIND
NP_BIND
NP_BIND
NP_BIND
Science [2]
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15-DEC-1998 (Rel.
16-OCT-2001 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGRFAMS; TIGR00491; aIF-2; 1. TIGRFAMS; TIGR00231; small_GTP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Methanococcus jannaschii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Archaea; Euryarchaeota;
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45; Conserv
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IPR004161; EFTU_D2.
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email to license@isb-sib.ch).
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. 37, Last sequence upd
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Matches 66
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01-NOV-1995 (Rel. 32, La
16-OCT-2001 (Rel. 40, La
Hypothetical 200.0 kDa p
YJL109C OR J0808.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Bordovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.; Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                               YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGREAMS; TIGRO0348; hsdR; 1.
Hypothetical protein; Complete |
SEQUENCE 1018 AA; 120992 MW;
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                                                                                            YJK9_YEAST
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InterPro; IPR004473;
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an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                         NYKKEIEKKYGKNVDELNKKWTEDFINKENPKILIVNKK----LLTGFDAPILKTIYIHQF
                                                                                                                                                                                                                                                                       RQEMAIQQSLGMRCQKMSMQ------AMVTIVTTKDTRMVTRMTTVIMRVITMDTL
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                                                                                              STANDARD;
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17.7%;
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HsdR.
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a protein in GZF3-IME2 i
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Pred. No. 10;
75; Mismatches
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                         Hypothetical AF0772.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0005732; C:small nucleolar ribonucleoprotein GO; GO:0030515; F:snoRNA binding activity; IPI. GO; GO:0030490; P:processing of 20S pre-rRNA; IMP. InterPro; IPR000357; HEAT_repeat. PROSITE; PS50077; HEAT_REPEAT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR;
SGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A 37.5 kb region of yeast chromosome X includes the SME1, and CSD3 genes, a TCP-1-related gene, an open reading frame to the DAL80 gene, and a tRNA(Arg)."; yeast 11:873-883(1995).

-i- SIMILARITY: BELONGS TO THE BAP28 FAMILY.

-i- SIMILARITY: Contains 1 HEAT repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=S288c / FY1679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical
REPEAT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
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 Archaeoglobus
Archaea; Eurya
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$0003645; YJL109C
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Z49384; CAA89404.1;
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46; Conser
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lobus fulgidus.
Euryarchaeota;
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                                                                 update)
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                                                   update)
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ne similar
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Best Local
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01-OCT-1994 (Rel. 3
01-OCT-1994 (Rel. 3
16-OCT-2001 (Rel. 4
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Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Retchum K.A., Dodson R.J., Gwinn M., Hickey B.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                    TTP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sections.com/discommended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commended-commende
Saccharomycetales;
NCBI_TaxID=4932;
                                                Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                          Saccharomyces cerevisiae (Baker's yeast).
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                                                                                                                                                                                                                                                                                  YEAST
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SEQUENCE 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus."; Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
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                                                                                                 protein (Mannan synthesis protein OR MNN2 OR YBR015C OR YBR0220.
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                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                               30, Last sequence update)
40, Last annotation update)
                         Saccharomycetaceae;
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Pred. No.
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                         Saccharomyces
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L outstation -
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HEP2_HUMAN
ID HEP2_H
AC P05546
AC P05540
DT 01-NOV
DT 01-NOV
DT 15-SEP
DE Hepari
DE (HLS2)
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15-SEP-2003 (Rel. 42
Heparin cofactor II (HLS2)
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Best Local
                                   HEP2_HUMAN
P05546;
01-NOV-1988
01-NOV-1991
15-SEP-2003
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CONFLICT
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Yeast 10:1111-1115(1994).
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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EMBL; Z35884; CAA84957.1;
PIR; S45870; S45870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
MEDLINE=95084638; PubMed=7992511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Type II
-!- SIMILARITY: TO YEAST YJL186W.
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                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO:0005794; C:Golgi apparatus; IDA.
GO:0000026; F:alpha-1,2-mannosyltransferase activity;
GO:0006486; P:protein amino acid 9lycosylation; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        $45870; $45870.
$0000219; MNN2.
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PK 165
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473
287
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                                                                                         STANDARD;
               . 09, Created)
. 20, Last sequence update)
. 42, Last annotation updat
II precursor (HC-II) (Prot
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287
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T., Schaaff
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                                                                                                                                                                                                                                                                                                                                                          27;
                                                                                                                                                                                                                                                                                                                                                       Score 96; DB 1
Pred. No. 7.4;
27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal-anchor.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
T-> K (IN REF. 1).
5 6C4FA1F4692A261C CRC64;
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EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M., Li Z., Thermann R., Brendel M. Schaaff-Gerstenschlaeger I.,
                        (HC-II) (Protease
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                          inhibitor leuserpin
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                        2)
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Ragg H., Pro
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MEDLINE-86077723; PubMed-3907702;
Griffith M.J., Noyes C.M., Tyndall J.A.,
"Structural evidence for leucine at the cofactor II.";
                                                             MEDLINE=90094412; PubMed=2104620;
Blinder M.A., Tollefsen D.M.;
"Site-directed mutagenesis of arginine
proposed glycosaminoglycan-binding site
J. Biol. Chem. 265:286-291(1990).
                                                                                                                                                                                                                                                                                                                           MEDLINE=91093260; PubMed=1985958; Church F.C., Pratt C.W., Hoffman M.; Leukocyte chemoattractant peptides
                                                                                                                                                                                                                                                                                                                                                                                                                             hLS2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhorn R.C., Tolletsen u.m.,
Inhorn R.C., Tolletsen u.m.,
"Isolation and characterization of
cofactor III.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ragg
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VARIANT OSLO HIS-208
MEDLINE-89174798; Pul
Blinder M.A., Anders:
                                                                                                                                                                                            van Deerlin V.M.D., Tollefsen D.M.;
"The N-terminal acidic domain of heparin
inhibition of alpha-thrombin in the prese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochemistry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                restriction fragment length Escherichia coli.";
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                FUNCTION OF N-TERMINAL ACIDIC DOMAIN MEDLINE=92041850; PubMed=1939083;
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF
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Nucleic Acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete nucleotide sequence of the II and mapping to chromosomal band 2: Biochemistry 30:1350-1357(1991).
                                                                                                                                              MUTAGENESIS OF ARG-122 AND LYS-204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=86242236;
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                                                                                                                                                                                  Biol.
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 Andersson
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                 PubMed=2647747;
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T.R.,
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Abildgaard
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e of
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σ.,
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                                                                                                                                                                                              cofactor II mediates the ence of glycosaminoglycans.";
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 Tollefsen
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D.M.;
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"Heparin affinity J. Biol. [11]
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the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
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Shaw N., Lane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genet. 23:373-373(1999).

FUNCTION: THROMBIN INHIBITOR ACTIVATED BY THE GLYCOSAMINOGLYCANS, FUNCTION: THROMBIN INHIBITOR ACTIVATED BY THE GLYCOSAMINOGLYCANS, HEPARIN OR DERMATAN SULFATE. IN THE PRESENCE OF THE LATTER, HC-II BECOMES THE PREDOMINANT THROMBIN INHIBITOR IN PLACE OF ANTITHROMBIN III (AT), ALSO INHIBITS CHYMOTRYPSIN, BUT IN A GLYCOSAMINOGLYCAN-INDEPENDENT MANNER.

FUNCTION: PEPTIDES AT THE N-TERMINAL OF HC-II HAVE CHEMOTACTIC ACTIVITY FOR BOTH MONOCYTES AND NEUTROPHILS.

TISSUE SPECIFICITY: EXPRESSED PREGOMINANTLY IN LIVER.

TISSUE SPECIFICITY: EXPRESSED THROMBIN INHIBITION.

DOMAIN: THE N-TERMINAL ACIDIC REPEAT REGION MEDIATES, IN PART, THE GLYCOSAMINOGLYCAN-ACCELERATED THROMBIN INHIBITION.

DISBASE: DEFECTS IN SERPINDI ARE ASSOCIATED WITH THROMBOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EM
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et. 22:231-238(1999)
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ne C.R., Lim
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Rolfe
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as its content is in
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Nemesh J., Z
zz R., Daley G
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Nemesh J., Ziaugr
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and for commercial
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G.Q.,
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AAA52641.1; CAA27218.1; AAA52642.1; ALT_INIT

EMBL; M58600; AAA52641.
EMBL; X03498; CAA27218.
EMBL; M12849; AAA52642.
EMBL; M33660; AAA36185.
PIR; A37924; A37924.
PDB; 1JMJ; 30-AUG-02.
PDB; 1JMO; 30-AUG-02. REPEAT
DOMAIN
MOD_RES
MOD_RES
CARBOHYD
CARBOHYD
CARBOHYD DOMAIN DOMAIN PRINTS; PR00780; LEUSERI SMART; SM00093; SERPIN; PR0SITE; PS00284; SERPII InterPro; IPR000295; Leuserpin2. InterPro; IPR000215; Serpin. Pfam; PF00079; serpin; 1. Genew; HGNC: MIM; 142360; REPEAT SIGNAL Disease mutation; Serpin; CHAIN Plasma; HGNC:4838; SERPIND1 Blood Serine protease inhibitor; Glycoprotein; Heparin-binding; Blood coagulation; Chemotaxis; Signal; Thrombophilia; 73 192 79 92 49 188 387 20 68 73 AAA36185.1; LEUSERPINII. SERPIN; 1 Sulfation; 19 499 79 97 83 97 212 79 92 49 188 387 GLYCOSAMINOGLYCAN-BINDING S
SULFATION.
SULFATION.
N-LINKED (GLCNAC. . .) (POT
N-LINKED (GLCNAC. . .) (POT
N-LINKED (GLCNAC. . .) (POT HEPARIN COFACTOR II.
CHEMOTACTIC ACTIVITY.
2 X 11 AA APPROXIMATE
RICH (ACIDIC) (HIRUDIN Repeat; Polymorphism; (HIRUDIN-LIKE)

3D-structure

REPEATS,

ASP/GLU

SITE

(POTENTIAL). (POTENTIAL).

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RESULT 11
PPID_BUCAP
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Best Local S
Matches 70
                  PPID_BUCAP STANDARD;
Q8X987;
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28-FEB-2003 (Rel. 41, Last
28-FEB-2003 (Rel. 41, Last
28-FEB-2003 (Rel. 41, Last
Peptidyl'prolyl cis-trans i
(Rotamase D);
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 aphidicola
                                                                                                                         EKNYNLVESLKLMGIRMLFDKNGNMAGISDQRIAIDLFKHQGTITVNEEGTQATTVTTV
                                                                                                                                                                                                  NIDPATQMMILNCIYFKGSWVNKFPVEMTHNHNFRLNEREVVKVSMMQTKGNFLAANDQE
                                                                                                                                                                                                                                                                                                              SAGNILQLFHGKSRIQRLNILNAKFAFNLYRVLKDQ~VNTFDNIFIAPVGISTAMGMISL 167
                                                                                                                                                                                                                                                                                                                            SVADLLGSFEGKRRL--LLITAPKAENNMYVQQRDEYLESFCKMATRKISVITIFGPVNN 83
                                                                                                                                          VIVYDLIDSMQLRRQEMAIQQS---LGMRCQKMSMQAMV---TIVTTKDTRMVTRMTTV
                                                                                                                                                             LDCDILQLEYVGGISMLIVVPHKMSGMKTLEAQLTPRVVERWQKSMTNRTREVLLPKFKL
                                                                                                                                                                                                                                      DLYIQKQFPILLDFKTKVREYY---FAEAQIADFSDPAFISKTNNHIMKLTKGLIKDALE
                                                                                                                                                                                                                                                        DF----FMVLTDVDLRVKQYYEVPITMKSVFDLID-TFQSRIKDMEKQKKEGIV----
                                                                                                                                                                                                                                                                          GLKGETHEQVHS-----ILHFKDFVNASSKYEITTIHNLFRKLTHRLFRRNFGYTLRSVN
                                                                                                                                                                                                                                                                                            STMKIDHFQLDNEKPMRVVDDEDLVD-------QRLISEL-RKEYGMT---YN
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483
486
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57070 MW;
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(subsp.
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19.5%;
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                           Last sequence update)
Last annotation updat
rans isomerase D (EC 5
                                                        Created)
                                                                                                                                                                                                                                                                                                                                                    63;
                                                                                                                                                                                                                                                                                                                                                 Score 95; DB:
Pred. No. 7;
63; Mismatches
Schizaphis graminum).
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MISSING (IN REF. 5).
R -> P (IN REF. 5).
C -> T (IN REF. 5).
S -> O (IN REF. 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLYCOSAMINOGLYCAN AFFINITY.
R->Q: GREATLY REDUCED THROMBIN
INHIBITION. NORMAL GLYCOSAMINOGLYCAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REACTIVE BOND (BY SIMILARITY).
A -> T (IN dbSNP:5905).
/FTId-VAR_011746.
                                                                                                                                                                                                                                                                                                                                                                                                                                               K->T: REDUCED HEPARIN- AND NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K->N: REDUCED HEPARIN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SULFATE-ACTIVATED INHIBITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R->W: GREATLY REDUCED THROMBIN
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                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                       3B0E353FE1F6DF05 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NORMAL THROMBIN INHIBITION
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                                                                          621
                            update)
(EC 5.2.1.
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AFFINITY FOR DERMATAN SULFATE;
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                                                                         RESULT 12
SRC1_YEAST
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                                              SRC1_YEAST (
Q03707; Q03712;
Q1-NOV-1997 (Re)
        SRC1 protein.
SRC1 OR YML034W/YML033W
                           01-NOV-1997 (Rel.
16-OCT-2001 (Rel.
15-SEP-2003 (Rel.
                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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57; Conserv
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621 AA;
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                                                                 STANDARD;
                           35,
40,
42,
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31
                           Last
Last
                                               Created)
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ramas I., Klasson L., Canbaeck B., Naeslund A.K., Eriksson A.-S. Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E., "50 million years of genomic stasis in endosymbiotic bacteria.", Science 296:2376-2379(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MCBI_TaxID=98794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS01096; PPIC_PPIASE_1; PROSITE; PS50198; PPIC_PPIASE_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00639; Rotamase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: Peptidylproline (omega=180) =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: T
SIMILARITY: BELONGS TO
STRONG, TO E.COLI PPID.
                                                                                                                                                                                                                              EYVSLIRKKLNTTY - - LINAISETDF - -
                                                                                                                                                                                                                                                                                                                                                                                                      LES----FCKMATRKISVITIFGPVNNSTMKIDHFQLDNE----KPMRVVDDEDLVDQ 110
QLKPNKFKIQCSNEEIKNWYKKN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NNYFNRDTTRYIAKVNGEEISFITLQKMYIDERKKQEKILGQDFEKIKKNKKFKEETYNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NKHFTQSPKKSVADLLG---SFEGKRRLLLITAPKAE------NNMYVQQRDEY
                                                                                                                                                                     EGIVCKEEVGGVLELFP-INGSSVVEREDVPAHLVKDIRNYFQ-----VSPEYFSMLLV
                                                                                                                                                                                                                                                                                    RLISELRKEYGMTYNDFFMVLTDVDLRVKQYYEVPITMKSVFDLIDTFQSRIKDMEKQKK 170
                                                                                                                                                                                                                                                                                                                                                ILSQLINNILLEQYTKRMNFNIQDNEIKKIIFNIPIFQENNEFNKKKYLNYLSSKNLTHY 150
                                                                                                               --IIKK----AIIKINPIINNQKVTE--
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355 F
74139 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.7%;
19.7%;
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                                                      --VKSWYPSPMWSMVIVYDLID--SMQLRRQEMAIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N: Type II membrane protein (Potential).
TO THE PPIC/PARVULIN FAMILY OF ROTAMASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 93;
Pred. No.
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EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5B7A89B253144C7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No. 13;
---IDKYSNQERRQYSIIQ
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                                                                                                                  ----KEINNYFDQHKNEFYTPEKFKISYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 621;
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ersson S.G.E.;
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                                                         .260
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(Baker's

sequence update) annotation updat

update)

PRT;

834

AA

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RESULT 13
IF2P_PYRAB
ID IF2P_P
AC Q9UZK7
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Best Local
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   IF2P_PYRAB
Q9UZK7;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T., Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S., Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Skelton J., Walsh S., Whitchead S., Barrell B.G.; "The nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The nucleotide sequence XIII.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane.
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EMBL; Z46659; CAA86622.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDENTIFICATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 387:90-93(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=9169872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomycetales; NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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                                                                                                            KARIEELVTQTMEKLKFQ----KIKSMSDPKENAYLSIVQLRDIFLSDIVDLKY
                                                                                                                                                                                                                                                                                                                                                                                                        KLKCKPDYKLAPSRLDFLEII-PAQGKCVK-----DDKK---
                                                                                                                                                                                                                                                                                                                                                                                                                                      ---C---KMATRKISVITIFGPVNNSTMKIDHFQLDNEKPMRVVDDEDLVDQRLISELR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LFGLWYREQRLLIGYCGHEVPSHRVSGNSFEFIQKLDNLLQDYRPKCIPCPPNGICYPYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLGSFEGKRRLLL-----ITAPKAENNM--YVQQRDEYLESF--------
                                                                                                                                                                                    FISKTRNFRSTSKKYIGMKCRFEREIYQTYKKFQRPIWLMFLLIVISKVIEIKLKNYYRK
                                                                                                                                                                                                                                                          DLWIQVIKDLTEEPE--ILWRQLSPTDNNIGG-----
                                                                                                                                                                                                                                                                                            DTFQSRIKDMEKQKKEGIVCKE-----EVGGVLELFPINGSSVVEREDVP---AHL---
                                                                                                                                                EMAIQQSLGMRCQKMSMQAMVTIVTTKDTRMVTRMTTVIMRVITMDTLTEQKY
                                                                                                                                                                                                                      -VKDIRNYFQVSPEYFSMLLVGKDGNVKSW--YPSPMWSM--VIVYDLIDSMQLR---RQ
                                                                                                                                                                                                                                                                                                                              EKSLEFLRAKNAQISCGDGKDDIESGMTEDALYQIFNEA----RAPWIRDDEFE--
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834 A
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17.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 92.5; D
Pred. No. 21;
'1; Mismatches
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214CA064ECE160F4 CRC64;
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     CHAIN
NP_BIND
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Qy

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Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte A Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C., Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.; A Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.; Ya integrated analysis of the genome of the hyperthermophilic rarchaeon Pyrococcus abyssi."; Mol. Microbiol. 47:1495-1512(2003).

Mol. Microbiol. 47:1495-1512(2003).

Mol. Microbiol. 47:1495-1512(2003).

THE BINDING OF THE FORMYLMETHIONINE-TRNA TO RIBOSOMES. SEEMS TO THE BINDING OF THE FORMYLMETHIONINE-TRNA TO RIBOSOMES. SEEMS TO THE FUNCTION ALONG WITH EIF-2 (BY SIMILARITY).

C. -!- MISCELLANDED WITH EIF-2 (BY SIMILARITY).

C. -!- MISCELLANDEOUS: THE INTEIN INTERRUPTS THE GTP BINDING SITE.

C. -!- SIMILARITY: BELONGS TO THE IF-2 FAMILY.

C. -!- SIMILARITY: BILONGS TO THE IF-2 FAMILY.

C. -!- SIMILARITY: IN THE INTEIN SECTION; BELONGS TO THE HOMING
                                                                                                                                                                                                                                               Pfam; PF00009; GTP_EFTU; 1.

Pfam; PF030144; GTP_EFTU_D2; 1.

ProDom; PD186100; TF2; 1.

SMART; SM00305; HintC; 1.

SMART; SM00305; HintN; 1.

TIGRFAMS; TIGR00491; alF-2; 1.

TIGRFAMS; TIGR01443; intein_Cterm; 1.

TIGRFAMS; TIGR01443; intein_Nterm; 1.

TIGRFAMS; TIGR01231; small_GTP; 1.

PROSITE; PS01176; TF2; FALSE_NEG.

PROSITE; PS01176; TF2; FALSE_NEG.

PROSITE; PS018; INTEIN_C_TER; 1.

PROSITE; PS50819; INTEIN_C_TER; 1.

PROSITE; PS50819; INTEIN_C_TER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000795; EF_GTPbind.
InterPro; IPR004161; EFFU_D2.
InterPro; IPR003586; Hedgehog_hintC.
InterPro; IPR003587; Hedgehog_hintN.
InterPro; IPR003187; Hedgehog_hintN.
InterPro; IPR006141; Intein.
InterPro; IPR006142; Intein.endonuc.
InterPro; IPR005225; Small_GTP.
InterPro; IPR004544; TIF_aIF-2.
Defai: DEF000004; TIF_aIF-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Probable translation initiation factor IF-2 [Contains: Pab infB intein (Pab IF2 intein)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ248286; CAB50050.1; PIR; E75093; E75093.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pyrococcus abyssi.
                                                                                                                                                                   Autocatalytic 
Endonuclease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAMAP; MF_00100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=29292;
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                                                                                                                                                                                                                                Initiation
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                                                                                                                                                                                                                             factor; Protein biosynthesis; GTP-binding;
                                                    21
415
472
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                                                                                                                                                                   Intron homing;
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                                                                                                                                       Protein splicing; Hydrolase; Nuclease ming; Complete proteome.

PROBABLE TRANSLATION INITIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermococci;
                  IF-2, 1ST PART (POTENTIAL).

PAB INFB INTEN (POTENTIAL).

PROBABLE TRANSLATION INTIATION FACTOR

IF-2, 2ND PART (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           There are no restrictions in as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermococcaceae;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIB1_BOVIN STANDARD;
PI0894;
01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NP_BIND
SEQUENCE
                                                                                                                                 the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                           "Determination of the primary structure of PLC-154 demonstrates diversity of phosphoinositide-specific phospholipase C activiti Cell 54:171-177(1988).
                                                                                       EMBL; J03137; AAA30702.1; -.
                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Katan M., Kriz R.W., Totty N., Philp R., Meldrum E.,
Knopf J.L., Parker P.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Last annotation update)
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase bet
(EC 3.1.4.11) (Phosphoinositide phospholipase C) (PLC-beta-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BOVIN
                               InterPro;
                                                            HSSP; P10688; 1DJX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=88270496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9913;
                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Phospholipase C-beta-1) (PLC-I) (PLC-154).
                                                                                                                     send
                                                                                                                                                                                                                                                                  COFACTOR: Calcium.

MISCELLANEOUS: THE RECEPTOR-MEDIATED ACTIVATION OF PLC-BETA 1 I MEDIATED BY TWO G-POTEIN ALPHA SUBUNITS, ALPHA-Q AND ALPHA-11.

SIMILARITY: DOMAINS TO THE TOTAL TOTAL ACTIVITY.
                                                                                                                                                                                                                                           OF PLC AND ARE ESSENTIAL FOR CATALYTIC SIMILARITY: Contains 1 C2 domain.
                                                                                                                                                                                                                                                                                                                       diacylglycerol
COFACTOR: Calc
                                                                                                                                                                                                                                                                                                                                                                  C ENZYMES.
CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHO
                                                                                                                                                                                                                                                                                                                                                     bisphosphate +
                                                                       A28822; A28822.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41;
                                                                                                                     an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
 ; IPR000008; C2.
; IPR001192; PI_PLC.
; IPR000909; PI_PLC_)
; IPR001711; PI_PLC_)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIAAPTPED--VEKAKQEILEQIERVVISTDKVGVIVKADTLGSLEALSKELQ-EKEIPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIDTFQSRIKDMEKQKKEGIVCKEEVGGVLELFP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LITAPKAENNMYVQQRDEYLESFCK--MATRKISVITIFGPVNNSTMKIDHFQLDNEKPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIEDYEEWVKEEEEKKKRELLSKVTFPGVIRLYPDERYVFRRSNPAIVGIEVIE 889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RVVD-----DEDLVDQRLISELRKEYGMTYNDFFMVLTDVDLRVKQYYEVPITMKSV-FD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         526 ·
992 AA;
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112224 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                    license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.6%;
PI_PLC_Xdom.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
                                                                                                                                                                                                                                                                                                                                                  1-phosphatidyl-1D-myo-inositol 4,5-
D-myo-inositol 1,4,5-trisphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36;
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Pred. No.
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9838BADA50E6F1C6 CRC64;
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                                                                                                                                                                   There are no restrictions ng as its content is in
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                                                                                                                                                                                                                                                             ACTIVITY.
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                                                                                                                                                 Usage
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RESULT 15
RNS2_SOLTU
ID RNS2_SOLTU
ID RNS2_S
AC 00179
DT 01-AE
DT 01-AE
DT 01-AE
DT 02-FE
DE Ribor
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Best Local :
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Pfam; PF00388; PI*PLC-Y; 1.
Pfam; PF00387; PI*PLC-Y; 1.
PFAM; PF00387; PI*PLC-Y; 1.
PRINTS; PR00390; PHPHLIPASEC.
PRODOM; PF001202; PI_PLC_Y; 1.
SMART; SM00239; C2; 1.
SMART; SM00148; PLCXG; 1.
SMART; SM00149; PLCXG; 1.
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Q01796;
Q1-APR-1993
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                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Strep
Spermatophyta; Magnoliophyta; e
Asteridae; lamiids; Solanales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-1993
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (S2-RNase).
Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ribonuclease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50004; C2_DOMAIN_2; 1.
PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
                                                                                                                                                                                                 locus
                                                                                                                                                                                                                        Kaufmann H., Salamini F., Thomp
"Sequence variability and gene
                                                                                                                                                                                                                                                                            MEDLINE=91246122; PubMed=2038308;
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4113;
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us of Solanum tuberosum.";
Gen. Genet. 226:457-466(1991).
Gen. Genet. 226:457-466(1991).
FUNCTION: SELF-INCOMPATIBILITY (SI) IS THE INHERITED ABILITY OF A FLOWERING PLANT TO PREVENT SELF-FERTILIZATION BY DISCRIMINATING BETWEEN SELF AND NON-SELF POLLEN DURING POLLINATION. IN MANY SPECIES OF THE SOLANACEAE, SELF-INCOMPATIBILITY IS CONTROLLED BY THE SINGLE, MULTIALLELIC LOCUS S: THIS STYLAR GLYCOPROTEIN IS ASSOCIATED WITH EXPRESSION OF SELF-INCOMPATIBILITY IN POTATO. CATALYTIC ACTIVITY: Two-stage endonucleolytic cleavage to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                He; Lipid degradation; Transducer; P)

316 467 DOMAIN X.

540 656 DOMAIN Y.

663 761 C2 DOMAIN Y.

331 BY SIMILARITY.

378 378 BY SIMILARITY.

887 887 PHOSPHORYLATION

1216 AA; 138714 MW; BEFR0917751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GMTYNDFFMVLTDVDLRVKQYY------EVPITMKSVFDLIDTFQS----RIKDM-EK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEKTAKKDNKKKSEPSSPDHV-SSTIEQDLAALDAEMTQKLVDLKDKQQQQLL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQDGYQKPTNKHFTQSPKKSVADLLGSFEGKRRLLLITAPKAENNMYVQQRDEY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NVKSWYPSPMWSMVIVYDLIDSMQLRRQEMAIQQSLGMRCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKKE----LKKKMDKKRQ-EKITEAKSKDKSQMEEEKTEMIRSYIQEVVQYIKRL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QKKEGIVCKEEVGGVLELFPINGSSVVEREDVPAHLVKDIRNYFQVSPEYFSMLLVGKDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LESFCKMATRKISVITIFGPVNNSTMKIDHFQLDNEKPMRVVDDEDLVDQRLISELRKEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QQKSFVKLQKKHY-----KEMKDLVKRHHKKTTDLI----KEHTTKYNEIQNDYLRRRAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S-2 precursor (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                 (Potato).
plantae: Streptophyta; Embryophyta;
panollophyta; eudicotyledons; core ev
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25,
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19.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
ursor (EC 3.1.27.1) (Stylar glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                     Thompson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 92;
Pred. No.
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                                                                                                                                                                                                                              structure
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                                                                                                                                                                                                                                                  R.D.;
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37;
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00530; RNASE_T2_1; PROSITE; PS00531; RNASE_T2_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001568; RNase_T2.
Pfam; PF00445; ribonuclease_T2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE RNASE T2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 łydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Extra TISSUE SPECIFICITY: PISTIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleoside 3'-phosphates and 3'-phosphooligonucleotides with 2',3'-cyclic phosphate intermediates.
                                                                                                                  111 DOYKKHGTCCLPRYNQL--
                                                                                                                                              115 ELRKEYGM----TYNDFFMVLTDVDLRVKQYYEVPITMKSVFDLIDTFQS------ 160
                                                        159 FKKIQDAIKTVTQEVPDLKCVENIQGVLELYEI 191
                                                                                    161 --RIKDMEK---QKKEGIVCKEEVGGVLELFPI 188
                                                                                                                                                                        54 I---HGLWPDKKPMRGQLQFCTSDDYIKFTPGSVLDALDHHWIQLKFEREIGIRDQPLWK 110
                                                                                                                                                                                                                                                                                                  al Similarity 47; Conserv
                                                                                                                                                                                                        86 MKIDHFQLDNEKPMR-----
                                                                                                                                                                                                                                         16
                                                                                                                                                                                                                                                                     26 SVADLLGSFEGKRRLLLITAPKAENNMYVQQRDEYLESFCKMATRKISVITIFGPVNNST 85
                                                                                                                                                                                                                                       SLSPIYGDFDYMQ--LVLTWPRSFC-----YPRGFCNRI------PPNNFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nuclease;
                                                                                                                                                                                                                                                                                                                                                            223 AA;
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55
112
116
                                                                                                                                                                                                                                                                                                               5.6%;
22.1%;
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Pred. No. 4.6;
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BY SIMILARITY.
RIBONUCLEASE S-2.
                                                                                                                                                                                                                                                                                                                                                            9BAFCCF15D737FDE CRC64;
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1 KKGGKTEQDGYQKPTNKHFT......DTLTEQKYVTLDSASFLCSC 320
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database :

pIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	و	8	7	6	S	.4	ω	2	_	Result No.
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a		21				.hypothetical prote	probable membrane	DNA helicase II BR	probable cytochrom	conserved hypothet	heparin cofactor I		ţy	TTP1 protein - yea		hypothetical prote		hypothetical prote			the	type I restriction	translation initia	hypothetical prote	4-alpha-glucanotra	hypothetical prote	pyr	protein - mo	Description

ALIGNMENTS

Qу Db	Qу Db	Qy Db	Qy Db	Qy Db	Оy	Query M Best Lo Matches	RESULT 1 JC7802 Urb protein C;Species: C;Date: 03- C;Accession R;Aoki, K: Biochem. Bi A;Title: Cl: A;Reference A;Accession A;Molecule A;Residues: A;Cross ref A;Note: Thr C;Comment: C;Generites: A;Gene: Urb A;Map posit C;Keywords: F;123/Doms F;123/Doms F;123/Doms F;123/534/R
240 MVIVYDLIDSMQLRRQEMAIQQSLGMRC 267 	180 GGVLELFPINGSSVVEREDVPAHLVKDIRNYFQVSPEYFSMLLVGKDGNVKSWYPSPMWS 239 	177EEV 179 765 QSLENFLSRFRWRRRLLVISAPNDEDWAYSQQLSALNGQACNFGLRHITILKLLGVGEEV 824	121 GMTYNDFFMYLTDVDLRVKQYYEVPITMKSVFDLIDTFQSRIKDMEKQKKEGIVCK 176 :	61 LESFCKMATRKISVITIFGPVNNSTMKIDHFQLDNEKPMRVVDDEDLVDQRLISELRKEY 120 	1 KKGGKTEQDGYQKPTNKHFTQSPKKSVADLLGSFEGKRRLLLITAPKAENNMYVQQRDEY 60 	Query Match 76.7%; Score 1261.5; DB 2; Length 949; Best Local Similarity 76.2%; Pred. No. 1.6e-83; Matches 250; Conservative 6; Mismatches 11; Indels 61; Gaps 1;	RESULT 1 Urb protein - mouse (Species: Mus musculus (house mouse) C;Species: Musculus (house mouse) C;Accession: JC7802 R;Aoki, K.; Sun, Y.; Aoki, S.; Wada, E. Biochem. Biophys. Res. Commun. 290, 1282-1288, 2002 A;Title: Cloning, expression, and mapping of a gene that is upregulated in adipose ti A;Reference number: JC7802; PMID:11812002; MUID:21670972 A;Rolecule type: mRNA A;Residues: JC7802; PMID:11812002; MUID:21670972 A;Molecule type: mRNA A;Residues: 1-949 caoks A;Cross-references: DDBJ:AB075019 A;Mote: Thise ATG codons are present in this ORF, the first Met residue is designated C;Comment: This protein, a secretory protein, whose expression is tissue-specific, pl C;Gene: Urb A;Map position: 16 C;Reywords: adipose tissue F;1-23/Domain: highly hydrophobic, signal sequence *status predicted <sig>F;1-23/Domain: highly hydrophobic, signal sequence *status predicted <sig>F;523-524/Region: cleavage recognition site by furin (Arg-Arg) *status predicted</sig></sig>

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE001437; PIDN:AAK78773.1; PID:g15023685; A;Experimental source: Clostridium acetobutylicum ATCC824 C;Genetics:
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A; Title: Genome Sequence and Comparative Analysis of the Solve A; Reference number: A96900; MUID:21359325; PMID:21359325
A; Accession: B96998
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                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, I., R.R.; Mckalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000
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C; Species: Clostridium acetobutylicum
                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE004416; GB:AE003853; NID:99658312; PIDN:AAF96782.1; GSPDB:GN00:A;Experimental source: serogroup O1; strain N16961; biotype El Tor
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A; Residues: 1-353 <HEI>
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A; Residues: 1-839 < KUR>
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                                                              NLYFSNDIMDSVLSIANTFKDS-NVQILTLFKALETRFDTAQLQQLTSL------IL
                                                                                                    NKHFTQSPKKSVADLLGSFEGKRRLLLITAPKAENNMYVQQRDEYLESFCKMATRKISVI
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H.; Dragoi, I.;
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A;Gene: malQ
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A; Residues: 1-489 <STO>
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                                                                                                    QAMVTIVTTKD 283
                                                                                                                                            QEIVKRHLNSNAMMVILPIQDWLAMSEQLRKEDAKSEQINIPANPYHYWNYRLHCQ----
                                                                                                                                                                                                                                                               DVP-----AHLVKDIRNYFQVSPE----YFSMLLVGKDGNVKSWY-PSPMW-----
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                                                            --LETLIDNQD 473
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                                                                                                                                                                                    -SMVIVYDLID----SMQLRRQEMAIQQ-
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18.1%;
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                                                                                                                                                                                                                                                                                                           -LACGEDLGMVPANVPDVMNHLNILRLIIERMPSDNRFVSPLN
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K.; Weissenbach,

324 301 272

221

Gaps

80

-SLGMRCQKMSM 272

464

356

197

154

255

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A; Kotatus; preliminary
A; Kolecule type: DNA
A; Kolecule type: DNA
A; Residues: 1-1134 <KAW>
A; Cross-references: GB:AJ248288; GB:AL096836; NID:g5458960; PIDN:CAB50554.1; PID:e151645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation initiation factor aIF-2 PH1095 [similarity] - Pyrococcus invitation (;Species: Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 28-Jul-2000 C;Accession: H71049 R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamot R;Kawarabayasi, Y.; Sawada, M.; Horikawa, T.; Kudoh, Y.; Yamazaki, J.; Kushid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence:
                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-1044 <ARNA
A;Residues: 1-1044 <ARNA
A;Residues: 1-1046 <ARNA
A;Rotes: 1-1046 <ARNA
A;Rote: this accession replaces an interim accession for a sequence replaced k
A;Rote: this accession replaces an interim accession for a sequence replaced k
C;Genetics:
A;Gene: PH1095
C;Guperfamily: translation initiation factor aIF-2 PH1095; translation elongat
C;Keywords: GTP binding
E;454-581/Domain: translation elongation factor Tu homology <ETU>
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A; Reference number: A75001
A; Accession: D75014
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C:Date: 20-Aug-1999 #sequence_revision
C:Accession: D75014
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DNA Res. 5, 55-76, 1998
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                                                                                                                                             772 VIAAPTPED---VERAKEEIMRQIESVV-ISTDKVGVIVKADTLGSLEALSKELQ-EKEI
                                                                                                    98 PMRVVD-----DEDLVDQRLISELRKEYGMTYNDFFMVLTDVDLR-VKQYYEVPITMKS-
                                                                                                                                                                                            42 LITAPKAENNMYVQQRDE----YLESFCKMATRKISVITIFGPVNNSTMKIDHFQLDNEK
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                    VFDLIDTFQSRIKDMEKQKKEGIVCKEEVGGVLELFP 187
                                                             PIRKADVGNISKTDVMEALSVKEENPKYGVILG--FNVKVNEDAKEVAKAKEVPIFVGNI
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25.5%;
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R;NG, W.V.; Kennedy, S.P.; Mahairas, G.G.; bergurse, C., Cruz, R.; Danson, M.J.; How Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.
A; Title: Genome sequence of Halobacterium species NRC-1.
A; Reference number: A84160; MUID:20504483; PMID:11016950
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A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus ja A;Reference number: A64300; MUID:96337999; PMID:8688087
                                                                                                                                                                   hypothetical protein Vng1843c [imported] - Halobacterium sp. NRC-1 C;Species: Halobacterium sp. NRC-1 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: E84335
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A; Start codon: GTG
C; Superfamily: type I site-specifi
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C;Genetics:
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A; Residues: 1-1018 <BUL>
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Superfamily:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     NYKKEIEKKYGKNVDELNKKWTEDFINKENPKILIVNKK----LLTGFDAPILKTIYIHQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----KFKAMVVAQDRKSCILFKKYLDEYLKEKIKNY--NENWTQVVITYIHNDDVEIE
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                                                                                                                                                                                                                                                                                                                                                   668
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                                                                                                                          Hough,
                                                           A.D.;
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                                                           Ebhardt,
                                                                                                                             D.W.;
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Merrick, J.M.; Glodek,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108;
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DNA Res. 5, 55-76, 1998
A;Title: Complete sequence (
A;Reference number: A71000;
A;Accession: B71009
A;Accession: B71009
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C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 28-Jul-2000
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M.: Ohfuku, Y.; Funahashi, T.;
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-218 <STO
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A; Residues: 1-728 <KAW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AP000006; NID:g3236133; PIDN:BAA30474.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GB: AE004437; NID: g10581289;
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Res. 5, 55-76, 1998
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                                             EAGSKVTFSVLLSAGEDSVISMDVREPRDWKACILVDGVRAQEIYLRRGETKVVNLILEI
                                                                                                            ESITLQLKVLPSSAGSHVVKFSING
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                                                                                                                                                                      YPYSEVTTEVNRSIMLPLTIFNNGTETVNVTFSVVNAPKDWDVKFYYQGIEIKKLKLREK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --IDHLQ-----QLDDAGLVESRVDDQRRKYFHTAENLRLEVQLSPFGYGAKSAYPA
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                                                                                                                                                                                                                                                                  FQLDNEKPMRVVDDEDLVDQRLISELRKEYGMTYND---FFMVLTDVDLRVKQ-----
                                                                                                                                                                                                                                                                                                 IGSYNARKGLFIVASWSSEGEKHVAKVGRYFEGF-----EVIT----VTNSSVTL--
                                                                                                                                                                                                                                                                                                                                                                                                                         Pyrococcus abyssi hypothetical protein PAB2446
-QOSLGMRCQKMSMQAMVTIVTTKDTRMVTRMTTVIMRVITMDTLTEQK
                                                                          -SPEYFSMLL-VGKDGNVKSWYPSPM-WSMVIVYDLIDSMQ--LRRQEMAI-----
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                                                                                                                                         -VCKEEVGGVLELFPINGSSVVEREDVPAHLVKDIRNYFQV------
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                                                                                                                                                                                                                                                                                                                                                                          Score 97;
Pred. No.
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Pred.
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                                                                                                          -DIYSFYVNVVQPKMEALKITAPILVQEA
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A; Molecule type: DNA
A; Residues: 1-1769 < RAF>
A; Cross-references: EMBL: X85021;
A; Note: the nucleotide sequence v
C; Genetics:
                                  hypothetical protein AF0772 - Arci
C;Specites: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_rev
C;Accession: D69346
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C;Keywords: transmembrane protein
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A; Title: A 37.5 kb region of yeast chromosome X includes
A; Reference number: S57357; MUID:96090136; PMID:7483851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-1769 <RAW>
A;Cross-references: EMBL:Z49384; NID:g1008292; PID:g1008293; MIPS:YJL109c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Date: 05-May-1995 #sequence_revision 01-Sep-1995
C;Accession: S53378; S56887; S57359
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                 R;Klenk,
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A; Residues: 1-1769 < RAS>
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A; Accession: $53378
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             H.P.; Clayton,
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 Quackenbush,
                 R.A.;
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                 Tomb,
                                                                                 Archaeoglobus fulgidus
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was submitted
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yeast chromosome
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                 J.F.; White,
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to the EMBL Data
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Nelson,
utton, G.
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Library, Fe
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   Gill,
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J.;

Lee,

N.H.;

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A;Title: The highly reduced ger
A;Reference number: A99082; MUJ
A;Accession: F90114
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-397 <DOUD>
A;Cross-references: GB:AJ01059;
C;Genetics:
C;Genetics:
A;Map position: 2
A;Genome: nucleomorph
C;Superfamily: ATP-dependent 20
C;Keywords: nucleomorph
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A; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Ka Smith, H.O.; Woese, C.R.; Venter, J.C.
A; Title: The complete genome sequence of the hyperthermophilic, sulf A; Reference number: A69250; MUID:98049343; PMID:9389475
A; Accession: D69346
A; Status: preliminary; nucleic acid sequence not shown; translation
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R;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, I Nature 410, 1091-1096, 2001
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Matches 61
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                                                                                                                                                                                                                                                                                      Similarity
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  VFDLIDTFQSRIKDMEKQKKEGIVCKEEVGGVLELF--PINGSSVVEREDVPAHLVKDIR 208 : :||: : | | | ::: | | :
                                                                                                                                                                                                               NNMYVQ-----QRDEYLESFCKMATRKISVITIFGPVNNSTMKIDHFQLDNEKPMRV-VD
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                                                                      NEGLIDKKNLN-LNSIYGVNKDSYYLISRLPPEYDFRVRAMEVDENPNQTYQDIGGLDNQ
                                                                                                                       DEDLVDQRLISELRKEYGMTYNDFFMVL---TDVDLRVK--
                                                                                                                                                                   NNNYEKIKLKDMKKELQEKIKSSSTLPHLVATISEIIYNQNRKIDGIILKTSNRLNIFLS
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20.2%;
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MUID:11323671; PMID:11323671
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                                                                                                                       -QYYEVPITMKS
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A;Accession: B45600
A;Status: nucleic acid sequence
A;Molecule type: DNA
A;Residues: 1-480 <NOL>
                                                                                          R;Nolte, D.; Knapp, B.
Mol. Biochem. Parasitol. 46,
A;Title: Partial sequences of
A;Reference number: A45600; N
                                                                                                                                                                                     asparagine-rich blood stage antigen (clone Pfa55-6) - Plasmodium falciparum C;Species: Plasmodium falciparum C;Decies: Plasmodium falciparum C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000 C;Accession: B45600; S27828
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A; Residues: 1-434 <STO>
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ce: strain IL1403
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0 9	QY 40 LLLITAPKAENNMYVQQRDEYLESFCKMATRKISVITIFGPVNNSTMKIDHFQLDNEKPM 99 : : : : : :
6;	Query Match 5.8%; Score 96; DB 2; Length 597; Best Local Similarity 24.2%; Pred. No. 25; Matches 44; Conservative 27; Mismatches 67; Indels 44; Gaps
	A;Gene: SGD:TTP1 A;Cross-references: SGD:S0000219; MIPS:YBR015c A;Map position: 2R C;Keywords: glycoprotein; transmembrane protein F;13-28/Domain: transmembrane #status predicted <tmm> F;29-597/Domain: extracellular #status predicted <ext> F;34,363,473/Binding site: carbohydrate (Asn) (covalent) #status predicted</ext></tmm>
	A; Status: not compared with conceptual translation A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-286, 'K', 288-597 < ROM> A; Cross-references: GB: U05211; NID: g500627; PIDN: AAA21860.1; PID: g500628 . C; Genetics:
I membrane	1111-1115, 1994 he nucleotide sequence of TTP1, a gene encoding a enumber: \$45595; MUID:95084638; PMID:7992511
	NT> EMBL: Z35884; NID: 9536213; PID: 9536214; ME: S488C
ur, A.; Bol	R;Entian, K.D.; Koetter, P.; Rose, M.; Li, Z.; Thermann, R.; Brendel, M.; Baur submitted to the Protein Sequence Database, August 1994 A;Reference number: S45862 A;Accession: S45870
	RESULT 15 \$45,870 TTP1 protein - yeast (Saccharomyces cerevisiae) N.Alternate names: protein YBR015c; protein YBR0220 N.Species: Saccharomyces cerevisiae C;Species: Saccharomyces cerevisiae C;Jate: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 28-May-1999 C;Accession: \$45,870; \$45,595
	Db 284 NNI 286
	Qy 291 TTV 293
290 . 283	Qy 236 PMWSMVIVYDLIDSMQLRRQEMAIQQSLGMRCQKMSMQAMVTIVTTKDTRMVTRM 29 :
235 241	Qy 178 EVGGVLELFPINGSSVVEREDVPAHLVKDIRNYFQVSPE'YFSMLLVGKDGNVKSWYPS 2:
177 190	Qy 125 -NDFFMVLTDVDLRVKQYYEVPITMKSVFDLIDTFQSRIKDMEKQKKEGIVCKE 1:
124 139 .	Qy 81 VNNSTMKIDHFQLDNEKPMRV
14;	Query Match 5.8%; Score 96; DB 2; Length 480; Best Local Similarity 21.8%; Pred. No. 19; Matches 53; Conservative 41; Mismatches 77; Indels 72; Gaps :
	A;Cross-references: EMBL:M59472; NID:g160105; PIDN:AAA29497.1; PID:g552186 A;Experimental source: isolate FCBR

Db	Qy	ф	Qy
164 PK 165	215 PE 216	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	160 SRIKDMEKQKKEGIVCKEEVGGVLELFPINGSSVVEREDVPAHLVKDIRNYFQVS 214

Search completed: July 24, 2003, 12:53:44 Job time: 18.7015 secs

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Result
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15 US-10-074-475-263

10 US-09-764-877-1151

15 US-10-102-806-717

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1753.524 Million cell updates/sec
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Sequence 7, Appli
Sequence 4, Appli
Sequence 9, Appli
Sequence 947, App
Sequence 263, App
Sequence 1151, Ap
Sequence 717, App
Sequence 6, Appli
Sequence 6, Appli
Sequence 486, App
Sequence 5229, Ap
Sequence 12125, A
Sequence 11205, A
Sequence 1, Appli
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09-759-010-6 -09-932-257A-27 -09-820-843A-73 -09-768-877-22	-09-974-298- -09-981-353- -10-177-293- -10-067-813- -09-925-300-	-10-128-714-8 -09-738-626-3 -09-779-307-1 -09-779-307-1	-10-083-357-1 -10-011-366-6 -10-208-948-1 -09-961-527A -10-163-214-2 -09-820-843A -10-128-714-8	US-10-136-891-2 US-10-120-687-1 US-10-116-949-2 US-10-116-949-4 US-10-014-101-10 US-10-014-101-35 US-10-128-714-8238 US-10-128-714-87-36 US-10-014-101-35
6, Appl 27, Ap 73, Ap 22, Ap	Sequence 41, Appl Sequence 158, App Sequence 258, Appl Sequence 4, Appli Sequence 1352, Ap	819 360 18, 17,	e 1343, e 6, App e 16, App e 5, App e 2, App e 15, App e 8540,	Sequence 2, Appli Sequence 1, Appli Sequence 2, Appli Sequence 4, Appli Sequence 10, Appl Sequence 35, Appl Sequence 8238, Ap Sequence 296, App Sequence 21183, A

ALIGNMENTS

RESULT 1 US-09-840-707A-7

GENERAL INFORMATION:

Sequence 7, Application US/09840707A Patent No. US20020077276A1

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                                                                                       Query Match
Best Local Similarity
Matches 320; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Fredeking, Terry M.
APPLICANT: Ignatyev, George M.
APPLICANT: Ignatyev, George M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING HEMORRHAGIC VIRUS
TITLE OF INVENTION: INVECTIONS AND OTHER DISORDERS
TILE REFERENCE: 24881-301C
CURRENT APPLICATION NUMBER: US/09/840,707A
CURRENT FILLING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: 09/562,979
PRIOR APPLICATION NUMBER: 09/562,979
PRIOR ETLING DATE: 2000-04-27
                                                                                                                                                                                                                                      OTHER INFORMATION: IL-1 receptor intracellular ligand protein OTHER INFORMATION: comprising amino acid sequence PUBLICATION INFORMATION: 5,817,476
PATENT DOCCIMENT NUMBER: 5,817,476
PATENT FILING DATE: 1995-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/198,210 PRIOR FILING DATE: 1999-04-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 320
TYPE: PRT
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  KKGGKTEQDGYQKPTNKHFTQSPKKSVADLLGSFEGKRRLLLITAPKAENNMYVQQRDEY
                           KKGGKTEQDGYQKPTNKHFTQSPKKSVADLLGSFEGKRRLLLITAPKAENNMYVQQRDEY
                                                                                          100.0%; ilarity 100.0%; Conservative 0
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                                                                                                                   Score 1645; DB 9;
Pred. No. 3.6e-154;
                                                                                            Mismatches
                                                                                            Indels
                                                                                                                                            Length
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RESULT 2
US-09-884-319-4
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Matches
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                                                   Query Match
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APPLICANT: Lin, Lih-Ling
Graham, James
                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 4:
                                  Local
                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/487,942 FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NOVEL INTERLEUKIN-1 RECEPTOR INTRACELLULAR LIGAND PROTEINS
                                                                                                                              MOLECULE TYPE: protein
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                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/884,319 FILING DATE: 18-Jun-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                             NAME: Brown, Scott A. REGISTRATION NUMBER: 32,724
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/083,516 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Cambridge
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: LEGAL AFFAIRS, GENETICS INSTITUTE, STREET: 87 CambridgePark Drive
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                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: GI5258
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                                                                                                                                                                                LENGTH: 320 amino acids
                 100.0%; ilarity 100.0%; Conservative 0,
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               Score 1645; DB 11;
Pred. No. 3.6e-154;
Mismatches 0;
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                                                     DB 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 7
LENGTH: 320
                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                          Query Match
Best, Local :
                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: IL-1 receptor intracellular ligand OTHER INFORMATION: comprising amino acid sequence PUBLICATION INFORMATION: 5.817,476 PATENT DOCUMENT NUMBER: 5.817,476 PATENT FILING DATE: 1995-06-07 PUBLICATION DATE: 1998-10-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/840,707
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: 09/562,979
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/198,210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/038,557A CURRENT FILING DATE: 2002-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING HEMORRHAGIC VIRUS TITLE OF INVENTION: INFECTIONS AND OTHER DISORDERS FILE REFERENCE: 24881-301D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Fredeking, Terry M. APPLICANT: Ignatyev, George M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1999-04-27
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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                                121 GMTYNDFFMYLTDYDLRVKQYYEVPITMKSVFDLIDTFQSRIKDMEKQKKEGIVCKEEVG
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                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                      100.0%;
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Pred. No. 3.6e-154;
; Mismatches 0;
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US-09-823-356-9
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US-09-823-356-9
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LENGTH: 950
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Best Local
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: HUMAN MEMBRANE SPANNING FILE REFERENCE: PF-0469-1 CON CURRENT APPLICATION NUMBER: US/19/823,356 CURRENT FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Tang,
                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2001-03-30 PRIOR APPLICATION NUMBER: 09/039,307 PRIOR FILING DATE: 1998 March 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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                                                                                                                               GMTYNDFFMVLTDVDLRVKQYYEVPITMKSVFDLIDTFQSRIKDMEKQKKEGIVCKEDKK 765
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             MVIVYDLIDSMQLRRQEMAIQQSLGMRC
                                    GGVLELFPINGSSVVEREDVPAHLVKDIRNYFQVSPEYFSMLLVGKDGNVKSWYPSPMWS
                                               GGVLELFPINGSSVVEREDVPAHLVKDIRNYFQVSPEYFSMLLVGKDGNVKSWYPSPMWS
                                                                                QSLENFLSRFRWRRRLLVISAPNDEDWAYSQQLSALSGQACNFGLRHITILKLLGVGEEV
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Baughn, Mariah R.
Shah, Purvi
Guegler, Karl J.
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Best Local
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NAME/KEY:
LOCATION:
                                                                                APPLICANT:
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REFERENCE: DEX-0313
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; OTHER INFORMATION: Xaa US-09-925-301-947
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PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. US20020052308A1
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TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA106
APPLICANT: Karra, Kalpana
APPLICANT: Cafferkey, Robert
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating
TITLE OF INVENTION: Genes and Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PCT/US00/05882 PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
                                                                                                                                                                      APPLICANT: Salceda, Susana APPLICANT: Macina, Roberto
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NAME/KEY: SITE
LOCATION: (312)
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                                                                                                                                                                                                                                                                                                                                                               247 SPMWSMVIVYDLIDSMQLRRQEMAIQQSLGMRC 279
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                                                                                                                                                    Hu, Ping
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o. US20030092898A1
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77.78;
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Pred. No. 3.7
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Ant
FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or fi
NUMBER OF SEQ ID NOS: 4031
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1151
LENGTH: 189
                                                                                                                                                    ; LOCATION: (189) ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-877-1151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-764-877-1151
; Sequence 1151, Application US/09764877
; Patent No. US20020147140A1
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; ORGANISM: Homo sapien
US-10-074-475-263
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CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: 60/268,292
PRIOR FILING DATE: 2001-02-13
NUMBER OF SEQ ID NOS: 295
SOFTWARE: PatentIn version 3.1
SEQ ID NO 263
LENGTH: 260
                                                                         Query Match
Best Local Similarity
Matches 118; Conserv
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Best Local Similarity
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LOCATION: (183)
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                               QSPKKSVADLLGSFEGKRRLLLITAPKAENNMYVQQRDEYLESFCKMATRKISVITIFGP
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EDKKQSLDNFLSRFRWRRRLLVISAPNDEDWAYSQQLSALSGQACNFGLRHITILKLLG-
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96.8%;
                                                                   31.2%; Score 513.5; DB 10; 42.6%; Pred. No. 9.1e-43; no. Mismatches 30;
                                                                                                                                                                                                                            equals any of the naturally occurring L-amino acids
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Pred. No. 8.3e-83;
1; Mismatches 5:
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                                                                                                             Length 189;
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RESULT 9 US-10-15 Sequen Sequen Public GENERA APPLI TITLE FILT CURRE CURRE CURRE PRIOR	ду Оу	Qy Qy	Query M Best Lo Matches	RESULT 8 US-10-10 Sequen Sequen Public GENERA APPLI TITLE FILE CURRE FILE CURRE PRIOR PRIO	Qy Db	Ωy	Db	γQ	, Q
SULT 9 -10-156-634A-4 -10-156-634A-4 Sequence 4, Application US/10156634A Publication NO. US20030013152A1 GENERAL INFORMATION: APPLICANT: DeJONG, Jeff L. APPLICANT: DeJONG, Jeff L. FILE OF INVENTION: Transcription Factors Related to TFIIA FILE REFERENCE: 119941-1092 CURRENT APPLICATION NUMBER: US/10/156,634A CURRENT FILING DATE: 2002-05-28 PRIOR APPLICATION UMBER: 09/326,529 PRIOR FILING DATE: 1999-06-04 NUMBER OF SEQ ID NOS: 20 SOFTWARE: PATENT Version 3.1 SEO ID NO 4	356 GRIREQQLSANIIEELRQFQRLTRSYENMYLIDKQGIDRDRYMEP 400 146 ITMKSVFDLIDTFQSRIKDMEKQKKEGIVCK 176 : : : : : : : : : : : : : :	26 SVADLLGSFEGKRRLLLITAPKAENNMYVQQRDEYLESFCKMATRKISVITIFGPVNNST E	y Match 9.0%; Score 147.5; DB 15; Length 431; Local Similarity 26.5%; Pred. No. 4.2e-06; hes 40; Conservative 29; Mismatches 67; Indels 15; Gaps 1	SULT 8 -10-102-806-717 Sequence 717, Application US/10102806 Publication No. US20030054421A1 GENERAL INFORMATION: APPLICANT: ROSEN et al. TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA103P1C1 CURRENT APPLICATION NUMBER: US/10/102,806 CURRENT FILING DATE: 2002-03-22 PRIOR APPLICATION NUMBER: US/9955,298 PRIOR APPLICATION NUMBER: PCT/US00/05881 PRIOR APPLICATION NUMBER: PCT/US00/05881 PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 2000-03-08 PRIOR FILING DATE: 1999-03-12 NUMBER OF SEQ ID NOS: 846 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 717 LENGTH: 431 TYPE: PRT ORGANISM: Homo sapiens	261 QSLGMRCQKMSMQAMVTIVTTKDTRMVTRMTTVIMRV 297 	201 AHLVKDIRNYFQVSPEYFSMLLVGKDGNVKSWYPSPMWSMVIVYDLIDSMQLRRQEMAIQ 260 	82	141 YYEVPITMKSVFDLIDTFQSRIKDMEKQKKEGIVCKEEVGGVLELFPINGSSVVEREDVP 200	VNNSTMKIDHFQLDNEKPMRVVDDEDLVDQRLISELRKEYGMTYNDFFMVLTDVDLRVKQ
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US-09-883-797-6
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Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Jaworski, Jan G.
APPLICANT: Post-Beittenmiller, Martha A.
APPLICANT: Todd, James
TITLE OF INVENTION: FATTY ACID ELONGASES
FILE REFERENCE: 07148/064001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/883,797
CURRENT FILING DATE: 2001-6-18
PRIOR APPLICATION NUMBER: 08/868,373
PRIOR FILING DATE: 1997-06-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 22
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                EYGMTYNDFFMVLTDVDLRVKQYYEVPITMKSVFDLIDTFQSRIKD-----MEKQKKEGI 173
                                                                                                                                                                                                                VDFSCYLPPSHLKVSIQTLMGHARRA
                                                                                                                                                                                                                                          ESF-CKM--ATRKISVITIFGPVNNSTMKIDHFQLDNEKPMRVVDDEDLVDQRLISELRK 118
                                                                                                                                                                                                                                                                        KGSKINVEDLQK-FSLHHTQNNLQTISLLLFLVVFVWILYMLTRPK-----FVYL
                                                                                                                                                                                                                                                                                                      KGGKTEQDGYQKPTNKHFTQSPKKSVADLLGSFEGKRRLLLITAPKAENNMYVQQRDEYL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGIVCKEEVGGVLELF-PINGSSVVERED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NDFFMVLTDVDLRV-----KQYYEVPITMKSVFDLIDTFQSRI----KDMEKQKK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRLSEPKVENFSVAGKIH--TVKIEHVSYTEKR--KYHSKTEVVHEPDIEQMLKLGSTSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRSQPKSGWSFMLRIPEKKNMMSSRQWGPIFLKVLPGGILQMYYEQGLEKPFKEIQLDPY 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FTQSPKKSVADLLGSFEGKRR------LLLITAPKAENNMYVQQ-----RDEYLESF
                                                                                                                    VCKEEVGGVLELFPIN---GSSVVEREDVPAHLVKDIRNYFQVSPEYFSMLLVGKDGNVK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TQIYCLCFVNGNLECFLTLNDLELPKRDE
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MVTRMTTVIMRVITMDTLTEQKYVTLDSASFLCSC 320
                                                        SWYPSPMWSMVIV--YDLIDSMQLRRQEMAIQQSL---GMRCQKMSMQAMVTIVTTKDTR 285
                                                                                                                                                    EAGMCWKN------KESDHLVD-FQEKILERSGLGQETYIFEGL
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20.3%;
                                                                                         FPLQQGMGASRKETEEVIFGALDNLFRNTGVKPDDIGILVV----NSS
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                                                                                                                                                                                                                                                                                                                                                 Score 95.5; DB 9; Pred. No. 0.72;
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                                                                                                                                                                                                                                                                                                                                    Mismatches 102;
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                             -----KSLNLGGMGCS----AGVIAVDVAKGLL
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                                                                                        204
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; NAME/KEY: SITE
; LOCATION: (145)
; OTHER INFORMATION: X
US-09-925-302-486
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                                                                                                                                    GENERAL INFORMATION:
                                                          APPLICANT:
APPLICANT:
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LENGTH: 510
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                                                                                                                                                    Patent No. US20020061569A1
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Best Local
                                            APPLICANT:
                                                                                                                 APPLICANT: Haselbeck,
                            APPLICANT:
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TITLE
               APPLICANT:
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OF.
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INVENTION: Identification of Essential Genes
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               Xu, H. Howard
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Sequence 5229, Application US/09815242
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PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                 411 EKNYNLVESLKLMGIRMLFDKNGNMAGISDQRIAIDLFKHQGTITVNEEGTQATTVTTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 GLKGETHEQVHS----ILHFKDFVNASSKYEITTIHNLFRKLTHRLFRRNFGYTLRSVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VIVYDLIDSMQLRRQEMAIQQS---LGMRCQKMSMQAMV---TIVTTKDTRMVTRMTTV 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              {\tt NIDPATQMMILNCIYFKGSWVNKFPVEMTHNHNFRLNEREVVKVSMMQTKGNFLAANDQE}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVADLLGSFEGKRRL--LLITAPKAENNMYVQQRDEYLESFCKMATRKISVITIFGPVNN 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLYIQKQFPILLDFKTKVREYY---FAEAQIADFSDPAFISKTNNHIMKLTKGLIKDALE
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                                                                                                                     Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
                                               Carr, Grant J.
Yamamoto, Robert T.
                                                                                                    Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----CKEEVGGVLELFPI----NGSSVVEREDVPAHLVKDIRNYFQVSP--
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                                                                                                                                                                                                                  Robert
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Best Local
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                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                Patent No.
                                                CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21
                                                                               TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                           APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
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SOFTWARE: FastSEQ for Windows Version
                                PRIOR APPLICATION NUMBER: 60/191,078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/206,848 FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NT FILING DATE: 2001-03-21
APPLICATION NUMBER: 60/191,078
FILING DATE: 2000-03-21
                FILING DATE:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/207,727
                                                                                                                                                                                                                                                                              INFORMATION:
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                                                                                                                                                                                                                                                                                              12125, Application US/09815242
o. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                    542 ALGASLQH---VIVDSEKDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TEKMKTRIDSLATQEEEYTYFFNGVKHILKAKNKELKGIHG-AVAEIIDVPSKLTQAIET
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                                                                                                                                                                        Carr, Grant J.
                                                                                                                                                                                                         Wall, Daniel
                                                                                                                                                                                                                       Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                      Xu, H. Howard
                                                                                                                                                                                       Trawick, John D.
                                                                                                                                                        Yamamoto, Robert T
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                2000-03-21
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22.7%;
60/206,848
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                                                                                                                                                                                                                                                                                                                                                                                                    558
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US-09-815-242-11205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
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SEQ ID NO 12125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. US20020061569A1
                                                                       PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Identification TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
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                  APPLICATION NUMBER:
                                                      APPLICATION NUMBER:
                                    FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 427 QLKDIQGQIKTTKKEYQQTNKELSAVDKEIKNIEKDLTDTKKAQNEYEE---KLYQAYRY 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11205,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 V--QQRDEYLESFCKMATRKISVITIFGPVNNSTMKIDHFQLDNEKPMRVVDD-----E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7
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59; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ERKKNQSETNARYEEEQENLIELLENISNEISEAQDTYKSLKSKQKELNAVIRELEEQLY 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TEKMKTRIDSLATQEEEYTYFFNGVKHILKAKNKELKGIHG-AVAEIIDVPSKLTQAIET 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDTFQSRIKDMEKQKKEGIVCKEEVGGVL-----ELFPINGSSVVEREDVPAHLVKDIRN 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EQDGYQKPTNKHFTQSPKKSV------ADLLGSFEGKRRLLLITAPKAENNMY 53
DATE:
                                                                                                                                                                                                                                                                                                                              Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                Yamamoto, Robert T
                                                                                                                                                                                                                                                                                                                                                                   Carr, Grant J.
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                                                                                                                                                                                                                                                                                                                                                                                                           Daniel
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                  60/257,931
                                                      60/253,625
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PRIOR FILING DATE: 2000-12-06

NUMBER OF SEQ ID NOS: 58

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1

LENGTH: 1618

TYPE: PRT

ORGANISM: Homo sapiens
US-09-963-875-1
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US-09-963-875-1
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11205
LENGTH: 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:

APPLICANT: Massachusetts General Hospital

TITLE OF INVENTION: Stem Cells of the Islets of Langerhans and Their Use in Treating

TITLE OF INVENTION: Mellitus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09963875
Patent No. US20020164307A1
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                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.6%; Score 91.5; D
Best Local Similarity 21.4%; Pred. No. 1.8;
                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/963,875
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US60/169082
PRIOR FILING DATE: 1999-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/238880 PRIOR FILING DATE: 2000-10-06 PRIOR APPLICATION NUMBER: US 09/731261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 17633/1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/215109 FILING DATE: 2000-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269 PEFTMLEYYQAYADYHDLMDNTEELLRKLAI 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166 RY------LDLISN------EESRRTFIIRSKVVAGIREYFISKGFMEVETPMLQ
670 EKENQEPLRSPEVGDEEALRPLTKENQEPLRSLEDE---NKEAFRSLEKE----NQEPLK 722
                                                                                     614 KPTGKEDTQTLQSLQKENQELMKSLEGNLETFLF--PGTENQELVSSLQENLESL--TAL 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209 VIPGGASARÞFVTHHNALDVDMYLRIAÞELYLKRLVVGGFERVFELNRNFRNEGVSVRHN 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  196 -----REDVPAHLVKDIRNYFQVSPE-YFSMLLVGKDGNV------KSWYPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 YYEVPITMKSVFDLIDTFQSRIKDMEKQKKEGIVCKEEVGGVLELFPINGSSVVE----- 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 --DLVD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 AEDGEILKEKGIEVQVAGRIMTRRAMGKATFITIQDMSGKIQLYVARDNLPEGVYKDDVG 110
                                      70 RKISVITIFGPVNNSTMKIDHFQLDNEKPMRVVDDEDLVDQRLISELRKEYGMTYNDFFM 129
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                                                                                                                           13 KPTNKHFT----QSPKKSVADLLGSFEGKRRLLLITAPKAENNMYVQQRDEYLESFCKMAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TWDLGDIVGIKGTLFKTKTDELTVKTTEVQLLTKALR-----PLPDKFHGLTDQEVRYRQ
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                                                                                                                                                                      5.4%; Score 89.5; Inilarity 25.3%; Pred. No. 15; Conservative 26; Mismatches
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Search completed: July 24, 2003, 13:14:52 Job time: 23.6724 secs

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Minimum
Maximum
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No.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title:
Perfect score:
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq.length: 2000000000
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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,
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    GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd
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US-09-257-581-7
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US-09-107-5328-6282
US-09-134-01C-4820
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US-09-198-4528-63
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US-09-188-188-63
US-08-845-1618-2
US-09-270-751-2
US-09-288-352-5891
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1 KKGGKTEQDGYQKPTNKHFTQSPKKSVADLLGSFEGKRRLLLITAPKAENNMYVQQRDEY 60

Score 1645; DB 1; Pred. No. 1.1e-177; ; Mismatches 0;

Length Indels

Gaps

0,

320;

Query Match 100.0%; 9 Best Local Similarity 100.0%; 1 Matches 320; Conservative 0;

RESULT 1 US-08-726-525-4 US-08-726-525-4 Sequence 4, Applicatt Patent No. 5789181 GEMERAL INFORMATION APPLICANT: Graha ITILE OF INVENTIO ITILE OF INVENTIO TITLE OF INVENTIO OTITLE OF INVENTIO ITITLE OF INVENTIO ITITLE OF INVENTIO OUNDATE OF SEQUENC CORRESPONDENCE AD ADDRESSEE: LEG STREET: 87 Cam COMPUTER READABLE MEDIUM TYPE: F MEDIUM TYPE: T MEGISTRATION NUM APPLICATION APPLICATION NUM APPLICATION APPL	28 85 29 85 29 84.5 31 84.5 32 83.5 33 83.5 83 83.5 83 82.5 36 82.5 39 82.5 81.5 81.5
ppplication 89181 RMATION: Lih- Lih- Lih- Lih- Graham, JNVENTION: SEQUENCES: SEQUENCES: EELEGAL A 87 Cambridge MUSA 100 A 100	5.2 793 3 5.2 1584 3 5.1 488 4 5.1 467 2 5.0 790 4 5.0 790 4 5.0 516 4 5.0 1151 4 5.0 1452 2 5.0 453 2 5.0 493 2 5.0 493 2 5.0 501 1
US/08726525 Ling ames NOVEL INTERLEUKIN-1 RECEPTOR INTERACELLULAR LIGAND PROTEINS AND BINDING 7 FAAIRS, GENETICS INSTITUTE, INC. gePark Drive PC-DOS/MS-DOS PC-DOS/MS-DOS PC-DOS/MS-DOS PC-DOS/MS-DOS PC-DOS/MS-DOS ATA: US/08/726,525 T-1996 5 A: 08/487,942 N-1995 ATION: A: 08/487,942 N-1995 ATION: A: 08/487,942 N-1995 SATION: A: 08/487,942 N-1995 SATION: B: 32,724 MBER: GI5258 ORMATION: 98-8824 -5851 NO: 4: ICS: ICS: acids	US-08-468-558-5 US-08-676-444-5 US-08-676-444-5 US-09-124-001C-4246 US-08-686-599A-17 US-09-107-532A-3777, US-09-723-129-2 US-09-723-129-2 US-09-107-532A-5205 US-09-1107-532A-5205 US-09-1107-532A-5205 US-09-134-001C-3242 US-09-134-001C-3242 US-08-685-599A-18 US-08-686-599A-18 US-08-686-599A-16 US-08-686-599A-16 US-08-686-599A-16 US-08-686-599A-16 US-08-451-715A-10
D INHIBITORS OF LIGAND	Sequence 5, Appli Sequence 6, Appli Sequence 4246, Appli Sequence 17, Appl Sequence 27, Appli Sequence 2, Appli Sequence 2, Appli Sequence 7156, Ap Sequence 5205, Ap Sequence 11, Appli Sequence 18, Appli Sequence 18, Appli Sequence 22255, A Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 10, Appli

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; MOLECULE TYPE: protein US-08-487-942-4
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                                                                 Matches
                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                             TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: NOVEL
TITLE OF INVENTION: INTRA
TITLE OF INVENTION: BIND
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CLASSIFICATION:
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121 GMTYNDFFMVLTDVDLRVKQYYEVPITMKSVFDLIDTFQSRIKDMEKQKKEGIVCKEEVG 180
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                                                                             Score 1645; DB 2; Pred. No. 1.1e-177;
                                                                 Mismatches
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Best Local Similarity
Matches 320; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Lin, L
APPLICANT: Graham
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NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: NOVE
TITLE OF INVENTION: INTR
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LESFCKMATRKISVITIFGPVNNSTMKIDHFQLDNEKPMRVVDDEDLVDQRLISELRKEY 120
                                                KKGGKTEQDGYQKPTNKHFTQSPKKSVADLLGSFEGKRRLLLLTAPKAENNMYVQQRDEY
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                                 KKGGKTEQDGYQKPTNKHFTQSPKKSVADLLGSFEGKRRLLLITAPKAENNMYVQQRDEY
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                                                                                                                                               US-09-083-516-4
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US-09-083-516-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application Patent No. 6300086
GENERAL INFORMATION:
                                                                                  Matches
                                                                                                 Query Match
Best Local
                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lin, Lih-Ling
APPLICANT: Graham, James
TITLE OF INVENTION: NOVEL
TITLE OF INVENTION: INTRAC
TITLE OF INVENTION: BINDIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: GITTELECOMMUNICATION INFORMATION: TELEPHONE: (617) 498-8224
                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                   NAME: Brown, Scott A. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
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                                                                                Local Sines 320;
                                                                                                                                                                                           TYPE:
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                                                                                               Similarity
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                                                                                                                                                                                        amino acid
                                KKGGKTEQDGYQKPTNKHFTQSPKKSVADLLGSFEGKRRLLLITAPKAENNMYVQQRDEY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87 CambridgePark Drive
                                                                                                                                                                                                                                                      (617) 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                Conservative
                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM PC compatible
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                                                                                                                                                          protein
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                                                                                             100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOVEL INTERLEUKIN-1 RECEPTOR
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                                                                              Score 1645; DB 4;
Pred. No. 1.1e-177;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Version #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEINS AND INHIBITORS OF LIGAND
                                                                                                         Length
                                                                                                            320;
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                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                 TELEFAX: (617) 227-59 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 02-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,7
                                                                                                                                                                                                     MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 227-7400
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CORRESPONDENCE ADDRESS:
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APPLICANT: Draetta, Giulio
TITLE OF INVENTION: CDK4 B
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CITY: Boston
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ZIP: 02109
                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                   TYPE: amino acid
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                                                                                                                                                                                                                                                                  LENGTH:
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                                                            QQRDEYLESFCK------FGPVNNSTMKIDHFQLDNEKPMRVVDDEDWVDQRLIS
                                                                             QQRDEYLESFCKMATRKISVITIFGPVNNSTMKIDHFQLDNEKPMRVVDDEDLVDQRLIS 114
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ELRKEYGLTYTDSSWCXQMWIXESSNTMRYQXQXSLCL----HLIDTFQSRIKDMEKQKK
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                                                                                                                                                                                                                                                                   358 amino acids
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internal
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63.2%;
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                                                                                                                        Score 396.5; DB 1
Pred. No. 3.1e-36;
Mismatches 22
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Length Indels

358; 19;

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US-09-326-529-4
                                                                                                                                  ; ORGANISM: Arabidopsis thaliana US-08-868-373-6
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US-08-868-373-6
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APPLICANT: Jaworski, Jan G.
APPLICANT: Post-Beittenmiller, Martha A.
APPLICANT: Todd, James
TITLE OF INVENTION: FATTY ACID ELONGASES
FILE REFERENCE: 07148/064001
                                                                                                                                                                CURRENT APPLICATION NUMBER: US/08/868,373
CURRENT FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
LENGTH: 504
TYPE: PRT
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SEQ ID NO 4
LENGTH: 1182
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Best Local
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                                                                    Matches
                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/326,529
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 19
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TITLE OF INVENTION: Transcription Factors
FILE REFERENCE: 119941-1053
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                                                                                   Local
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45; Conserv
                                 2 KGGKTEQDGYQKPTNKHFTQSPKKSVADLLGSFEGKRRLLLITAPKAENNMYVQQRDEYL
                                                                                   Similarity
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KGSKINVEDLQK-FSLHHTQNNLQTISLLLFLVVFVWILYMLTRPK----
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Pred. No. 0.02;
                                                                                 Score 95.5; DB Pred. No. 0.068;
                                                                  Mismatches
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                                                                                               DB 4; Length 504;
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                                                                  Indels 113;
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SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 5
LENGTH: 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application Patent No. 6207419 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 5470-232
CURRENT APPLICATION NUMBER: US/09/257,581
CURRENT FILING DATE: 1999-02-25
EARLIER APPLICATION NUMBER: 60/076,210
EARLIER FILING DATE: 1998-02-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Church, Frank C. APPLICANT: Bauman, Susannah J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: THROMBIN INHIBITORY AGENTS AND METHODS OF USING
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                                    241 VIVYDLIDSMQLRRQEMAIQQS---LGMRCQKMSMQAMV---TIVTTKDTRMVTRMTTV 293
                                                                                                                                                         280 NIDPATQMMILNCIYFKGSWVNKFPVEMTHNHNFRLNEREVVKVSMMQTKGNFLAANDQE
                                                                                                                                                                                                                                                                                                                  168 GLKGETHEQVHS-----ILHFKDFVNASSKYEITTIHNLFRKLTHRLFRRNFGYTLRSVN 222
                                                                                                                                                                                                                                                                                                                                                                                              109 SAGNILQLFHGKSRIQRLNILNAKFAFNLYRVLKDQ-VNTFDNIFIAPVGISTAMGMISL 167
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70; Conservative
EKNYNLVESLKLMGIRMLFDKNGNMAGISDQRIAIDLFKHQGTITVNEEGTQATTVTTV
                                                                           LDCDILQLEYVGGISMLIVVPHKMSGMKTLEAQLTPRVVERWQKSMTNRTREVLLPKFKL
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                                                                                                                                                                                                                                                                            DF----FMVLTDVDLRVKQYYEVPITMKSVFDLID-TFQSRIKDMEKQKKEGIV-----
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                                                                                                                -----EY---FSMLLV--GKDGNVKS------WYPS------PMWSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.7%; Score 94; DB
19.5%; Pred. No. 0.1;
ative 63; Mismatches
                                                                                                                                                                                              -CKEEVGGVLELFPI----NGSSVVEREDVPAHLVKDIRNYFQVSP--
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RESULT 9 US-09-257-581-7

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US-09-107-532A-6282
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Best Local S
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SOFTWARE: PATENTIN VER. 2.0
SEQ ID NO 7
LENGTH: 505
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CURRENT FILING DATE: 1999-02-25
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APPLICANT: Bauman, Susannah J.
TITLE OF INVENTION: THROMBIN INHIBITORY AGENTS AND METHODS OF USING SAME FILE REFERENCE: 5470-232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EARLIER APPLICATION NUMBER: 60/076,210 EARLIER FILING DATE: 1998-02-27
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                                                       SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lynn A Doucette-Stamm TITLE OF INVENTION: NUCLEIC ACID
    PRIOR
                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  400 EKNYNLVESLKLMGIRMLFDKNGNMAGISDQRIAIDLFKHQGTITVNEEGTQATTVTTV 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 SAGNILQLFHGKSRIQRLNILNAKFAFNLYRVLKDQ-VNTFDNIFTAPVGISTAMGMISL
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70; Conservative
APPLICATION NUMBER: US/09/107,532A FILING DATE: 30-Jun-1998 APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LDCDILQLEYVGGISMLIVVPHKMSGMKTLEAQLTPRVVERWQKSMTNRTREVLLPKFKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIDPATQMMILNCIYFKGSWVNKFPVEMTHNHNFRLNEREVVKVSMMQTKGNFLAANDQE 339
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                                                                                                OPERATING SYSTEM: <Unknown>
                                                                                                                  COMPUTER: PC
                                                                                                                                                                                                                                                     ADDRESSEE: GENOME THERAPEUTICS CORPORATION STREET: 100 Beaver Street
                                                                                                                                    MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                STATE: Massachusetts
                                                                                                                                                                                                                                    CITY: Waltham
                                                                                                                                                                             02354
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                                                                                                                                                                                                                                                 100 Beaver Street
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Pred. No. 0.1;
63; Mismatches
                                                                                                                                                                                                                                                                                                                                and David Bush
AND AMINO ACID SEQUENCES RELATING
FAECIUM FOR DIAGNOSTICS AND THERAF
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RESULT 11
US-09-134-001C-4820
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ORGANISM: Staphylococcus epidermidis US-09-134-001C-4820
                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                SEQ ID NO 4820
LENGTH: 1211
                                                                                                                                                                                                                                                                                                                                                                           Sequence 4820, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                        PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08
                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                   FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (781)893-8277 INFORMATION FOR SEQ ID NO: 6282:
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SEQUENCE DESCRIPTION: SEQ ID NO: 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: YES ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: July 2, 1 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   273 QLLIELDHTSQSYTLNHNEIGRVRGFQTEVEEMERQNEQMIPQIRQHEIPYSEVRTFYKT 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      230 RETADLIDS-----LYDILEREMEAQRYVKTNQSTIAEYIKHTTK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 KSVADLLGSFEGKRRLLLITAPKAENNMYVQQRDEYLESFCKMATRKISVITIFGPVNNS 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PMWSMVIVYDLIDSMQLRRQ 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VFKVLEDIE----KQQVEIDDSLHELRKGEKEAQEKIDTFEFKLRSLKRFVEKQRLPGL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEMVLTDVDLRVKQYYEVPITM-----KSVFDLIDTFQSRIKDM----EKQKKEGIVC 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TM--KIDH----FQLDNEKPMRV------VDDEDLVDQRLISELRK-----EYGMTYND 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----THDLVDAAALTEQ 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEEVGGVLELFPINGSSVVEREDVPAHLVKDIRNYFQVSPEYFSMLLVGKDGNVKSWYPS 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Ariniello, Pamela Deneke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/051571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 14 May
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---PNDYLEFFFVATDRIEE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/085,598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH: 514 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 89.5; DB Pred. No. 0.34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -LSVVLNKIRVNMEEVNRLVALCEEDLELLDKK 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6282:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87;
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Query Match
Best Local Similarity

Matches

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US-07-853-913-4 Sequence 4, Applic Patent No. 5338839

GENERAL INFORMATION:

CLASSIFICATION: FILING DATE: COUNTRY:

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INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 07/003,000 FILING DATE: 25-OCT-1990 PRIOR APPLICATION DATA: US 07/201,762
                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Rel. CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS: hamilton, Brook, Smith & Reynolds,
                                                                                                                                                                                                                                                                                                                FILING DATE: 22-FEB-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/660,412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                        SEQUENCE CHARACTERISTICS:
                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 617-861-6240
                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/180,548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: McKay, Ronald I
APPLICANT: Lendahl, Urban
                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                           APPLICATION NUMBER: US 07 FILING DATE: 02-JUN-1988
                                                                                                                                   NAME: Granahan, Patricia REGISTRATION NUMBER: 32,
                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            551 VINVPSEMTQAIETALGASLQH --- VIVDNEKDG 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 REDVPAHLVKDIRNYFQVSPEYFSMLLVG--KDG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    504 RYNEKLKSRIDSLATQEEDYTYFFNGVKHILKAKDK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 EVPITMKSVFDLIDT-----FQSRIKDMEKQKKEGIVCKEEVGGVLELFPINGSSVVE 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         444 VEAFNQLKDIQQNITQTQKEYQSSKKSMEKVEQNIQQLEQQLTDSKRLLSEYENKLYQAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 VD------QRLISELRKEYGMT------YNDFFMVLTDVDLRVKQYY 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 392 ISDEQHDEKLEEI-----KNSYYTLMSEQSVVNNDIRFLEHTINENEAKKSRL--DSRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          332 ERKKNQSETNARYEEELDNLESQIDSIKNEKAQNEKLLADLKNKQKQLNKEVQELESLLY 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 V--QQRDEYLESFCKMATRKISVITIFGP---VNNSTMKIDHPQLDNE-KPMRVVDDEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 EQDGYQKPTNKHFTQ------SPKKSVADLLGSFEGKRRLLLITAPKAENNMY
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                                                              617-861-9540
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22.3%;
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                                                                                                                  MIT-4641AAAA
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Pred. No. 1
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Patent No. 5639651
                                                                                                                Matches
                                                                                                                                 Query Match
Best Local :
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Best Local 9
                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 0076
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: Clark, Paul C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: GAP-RELATED
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TELEFAX: 200154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: AU CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: MA
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                                                                                                                                                                                                                           TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street
                                                                                                                                                                                                                                                           LENGTH:
                                        691 KGGYYYYHNLETQEGGWDEPPN--FVQNSMQLSREEIQSSISGVTAAYNREQLWLANEGL 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  723 TLEEEDQSIVRPLETE-NHKSLRSLEEQDQETLRTLEKETQQ 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 VLTDVDLRVKQYYEVPITMKSVFDLIDTFQSRIKDMEKQKKE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           670 EKENQEPLRSPEVGDEEALRPLTKENQEPLRSLEDE---NKEAFRSLEKE----NQEPLK 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 614 KPTGKEDTQTLQSLQKENQELMKSLEGNLETFLF -- PGTENQELVSSLQENLESL -- TAL 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 RKISVITIEGPVNNSTMKIDHFQLDNEKPMRVVDDEDLVDQRLISELRKEYGMTYNDFFM 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 KPTNKHFT----QSPKKSVADLLGSFEGKRRLLLITAPKAENNMYVQQRDEYLESFCKMAT 69
                                                                            2 KGG-----KTEQDGYQKPTNKHFTQSP-----KKSVADLLGSFEGKRRLL----L
                                                                                                                73;
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                                                                                                                                   Similarity
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                                                                                                                                                                                                                                          amino acid
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                                                                                                                                                                                                                                                             1657 amino acids
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                                                                                                                                                                                                                             linear
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                                                                                                                Conservative
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                                                                                                                                 5.4%; Score 89.5;
18.2%; Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lawrence
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Pred. No. 2
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                                                                                                                                                  DB 1;
                                                                                                                128;
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                                                                                                                                                  Length 1657;
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                                                                                                                Indels 131;
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-QQRDEYLESFCKMATRKIS 73
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                                                                                                                Gaps
                                                                              42
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RESULT 15
US-08-680-326-41
US-08-680-326-41; Sequence 41, Application US/08680326; Patent No. 5925733; GENERAL INFORMATION:
APPLICANT: ROSE, TIMOTHY M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 63
LENGTH: 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fractitle of INVENTION: thereof and uses thereof, in particular for the diagnosis, TITLE OF INVENTION: and treatment of infection FILE REFERENCE: 97.10-003-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/198,452A CURRENT FILING DATE: 1998-11-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Chlamydia pneumoniae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 279 ETCLYKSLTKSYRDTFCDYKRAKIL-----PDENNSARAEQRFREVKDHWEDLNETVFW 332
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21.5%; Pred. No. 0.55;
tive 36; Mismatches
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Search completed: July 24, Job time: 16.1534 secs
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SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 29
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEPAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,
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STATE: California
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                                                           QNFKSHGFGCDIIDM 468
                                                                                        AIQQSLGMRCQKMSM 272
                                                                                                                                                   QVSPEYF-SMLLVGKD------GNVKSWYPSPMWSMVIVYDLIDSMQLRRQEM
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                                                                                                                      SVKPQLFKAQILMGQDILKANYLKLLEGIGSVLAQAKSTMAKMCTIKERIDSYRKMKDTV
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TODARO, GEORGE J.
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20.5%;
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              2003,
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
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Gapop 10.0 , Gapext 0.5
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1645
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1: /SIDS1/gcgdata/g
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| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1982.DAT: *
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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2002
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003
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AAB37795
AAX33298
ABB61194
ABR47911
ABR00162
AAB43503
ABJ18424
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Type 1, p80 IL-1-r
Human interleukin-
Human membrane spa
Human secreted pro
Human gene 152 enc
Human cancer assoc
Human breast cance
Breast specific re
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RESULT 1
AAW1990
ID AAW1990
ID AAW1990
ID 27-A
AC AAW1
XX 27-A
DT 27-A
DT 27-A
DT 19-C
XX IL:
KW INT.1
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ALIGNMENTS

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WPI; 1997-052315/05. N-PSDB; AAT71217. Interleukin-1 receptor intracellular ligand proteins and related DNA (GEMY) GENETICS INST INC. 95US-0487942 96WO-US06363

Result

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                                                          27-APR-1999;
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                                                                                                                                         WO200064479-A1
                                                                                                                                                                                           inflammation; infection; sepsis; cachexia; autoimmune d cardiovascular disorder; chronic myelogenous leukaemia; multiple sclerosis; inflammatory bowel disease; Crohn's
                                                                                                                                                                                                                                  antiinflammatory; haemostatic; antibacterial; immunosuppressive;
immunomodulator; cardiant; cytostatic; neuroprotective; respirat
                                                                                                                                                                                                                                                                                       Human interleukin-1 receptor intracellular ligand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW19990 represents a protein that has interleukin-1 receptor (IL-1-R) intracellular ligand activity. IL-1-R intracellular ligand proteins seed to screen for agents (and the ligand proteins) that are capable of inhibiting or blocking the binding of an IL-1-R, intracellular ligand to the intracellular domain of IL-1-R, i.e. inhibitors of IL-1 activity. Such agents can be used to treat inflammatory conditions.
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                                                                                                                                                                                                                                                             interleukin-1; IL-1; IL-lalpha; IL-lbeta; IL-1 receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KKGGKTEQDGYQKPTNKHFTQSPKKSVADLLGSFEGKRRLLLITAPKAENNMYVQQRDEY
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ilarity 100.0%;
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     Ignatyev GM;
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                                                                                                                                                                                                                                The present sequence is given in a specification relating to novel compositions and methods containing tetracycline or tetracycline-like compounds for treating and/or preventing acute inflammatory responses a diseases. Such diseases include acute inflammatory conditions associate with viral haemorrhagic diseases (including diseases caused by Bunyaviridea, Filoviridae, Flaviviridae or Arenaviridae viruses), parasitic diseases, bacterial infections, sepsis, cachexia, autoimmune disorders, acute cardiovascular events, chronic myelogenous leukaemia a transplanted bone marrow-induced graft-versus-host disease, septic shoc multiple accomplex-induced collits, cerebrospinal fluid inflammation,
                                                                                                                                                                                systemic inflammatory response syndrome (SIRS), adult respiratory distress syndrome (ARDS), acute liver failure, inflammatory bowel
                                                                                                                         Sequence
                                                                                                                                                                                                                      multiple sclerosis, inflammatory responses associated with trauma,
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                                                                                                                                                               Crohn's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              compositions comprising tetracycline or tetracycline-like unds for the treatment and/or prevention of acute inflammatory assess and diseases, e.g. septic shock and immune complex-induce
                                                              Similarity
      KKGGKTEQDGYQKPTNKHFTQSPKKSVADLLGSFEGKRRLLLITAPKAENNMYVQQRDEY
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                                                                                                                       GMTYNDFFMVLTDVDLRVKQYYEVPITMKSVFDLIDTFQSRIKDMEKQKKEGIVCKEEVG
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DTLTEQKYVTLDSASFLCSC
                   DTLTEQKYVTLDSASFLCSC
                                                                             GVLELFPINGSSVVEREDVPAHLVKDIRNYFQVSPEYFSMLLVGKDGNVKSWYPSPMWSM
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AAY33298
standard;
Protein;
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ΑA

Human membrane spanning

26-NOV-1999

(first

entry)

protein MSP-5.

Membrane spanning protein; treatment; diagnosis; neoplastic prevention; human; immunological disorder; reproductive disc MSP-5

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WO9946380-A2

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Guegler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes novel human membrane spanning proteins (MSPs), and the polynucleotides encoding them. The products of the invention are used to diagnose, prevent and treat neoplastic, immunological and reproductive disorders. This sequence represents the human membrane spanning protein MSP-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-551409/46.
N-PSDB; AAZ09839, AAZ09840.
                                                                                                                                                                           Human membrane
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                                                                    Homo
                                                                                                                                    Atherosclerosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKGGKTEQDGYQKPTNKHFTQSPKKSVADLLGSFEGKRRLLLITAPKAENNMYVQQRDEY
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                                                                                                         antiarteriosclerotic; marker; cardiovascular;
g protein; MSP-5; human.
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Matches 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to the use of a polynucleotide differentially expressed in ruptured and stable atherosclerotic plaques as a marker for atherosclerosis, where the polynucleotides can be selected from the sequences shown in ABQ79517-19. The polynucleotides are useful as a marker of atherosclerosis, which may be used: (i) in the diagnosis, prevention and treatment of atherosclerosis; (ii) as serum/plasma markers to screen patients at risk for plaque instability to evaluate the effects of other treatments; (iii) in the preparation of vector molecules for the expression of the encoded protein in host cells; and (iv) in the polynucleotides, the encoded proteins or analogues of the gene. The polynucleotides, the encoded proteins or antibodies against the proteins may be used to target other therapeutics to an unstable plaque.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of a polynucleotide differentially expressed in ruptured and atherosclerotic plaques as a maker for atherosclerosis, useful ir treating, diagnosing or preventing atherosclerosis:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modulation of the expression of the polynucleotide can increase plaque stability and therefore inhibit the progression of atherosclerotic cardiovascular disease. Modulators may be used to prepare pharmaceuticals for atherosclerotic disorders. The present sequence represents a membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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267; Conserv
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                                                                                                                                                                                                                                                  GMTYNDFFMYLTDVDLRVKQYYEVPITMKSVFDLIDTFQSRIKDMEKQKKEGIVCK----
              MVIVYDLIDSMQLRRQEMAIQQSLGMRC
                                                                             GGVLELFPINGSSVVEREDVPAHLVKDIRNYFQVSPEYFSMLLVGKDGNVKSWYPSPMWS
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                                                             GGVLELFPINGSSYVEREDVPAHLVKDIRNYFQVSPEYFSMLLVGKDGNVKSWYPSPMWS
                                                                                                                          QSLENFLSRFRWRRRLLVISAPNDEDWAYSQQLSALSGQACNFGLRHITILKLLGVGEEV
                                                                                                                                                                                          GMTYNDFFMVLTDVDLRVKQYYEVPITMKSVFDLIDTFQSRIKDMEKQKKEGIVCKEDKK
MVIVYDLIDSMQLRRQEMAIQQSLGMRC
                                                                                                                                                                                                                                                                                                                                                                                                                                               950 AA;
                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human secreted proteins, useful for detecting, preventing, diagnosing, prognosticating, treating and/or ameliorating cardiovascular disorders such as arrhythmia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic;
vulnerary; antiinflammatory; nootropic; neuroprotective;
                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 13;
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19-JUL-2001; 2001US-306171P.
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                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                          format and is available from WIPO at
       121
                                                                                                                                                                                               267;
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                                                                                                                                                                                                              Similarity
                                                                                                                                        KKGGKTEQDGYQKPTNKHFTQSPKKSVADLLGSFEGKRRLLLITAPKAENNMYVQQRDEY
       GMTYNDFFMVLTDVDLRVKQYYEVPITMKSVFDLIDTFQSRIKDMEKQKKEGIVCK----
                                                               LESFCKMATRKISVITIFGPVNNSTMKIDHFQLDNEKPMRVVDDEDLVDQRLISELRKEY
                                                                                                                 KKGGKTEQDGYQKPTNKHFTQSPKKSVADLLGSFEGKRRLLLITAPKAENNMYVQQRDEY
                                            LESFCKMATRKISVITIFGPVNNSTMKIDHFQLDNEKPMRVVDDEDLVDQRLISELRKEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID 802; 1881pp; English.
                                                                                                                                                                                                                                                                                                                                         sequence data for this patent was
                                                                                                                                                                                                                                                                    950 AA;
                                                                                                                                                                                             Conservative
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Pred. No. 8.4e-132;
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                                                                                                                                                                                             Mismatches
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                                  the use of the secreted proteins in drug screening, and recombinant vectors and host cells comprising a nucleic acid of the invention. The secreted proteins, nucleic acids encoding them, antibodies or antibody fragments specific for the secreted proteins, and modulators of protein activity are useful for diagnosing, treating, ameliorating or preventing digestive disorders. Such conditions include disorders of the mouth, oesophagus, stomach, small intestine, large intestine, liver, biliary tract and pancreas, and include cancers of these organs and tissues. The secreted proteins and their nucleic acids may also be used in the
                                                                                                                                                                                                       protein genes, and ABP00011-ABP00299 represent the proteins they encode. ABZ71479-ABZ71540 represent human secreted protein genomic fragments. The invention also encompasses antibodies specific for the secreted proteins,
                                                                                                                                                                                                                                                                                                 Claim 13; Page 1038-1041; 1216pp;
                                                                                                                                                                                                                                                                                                                                 New human secreted proteins and nucleic acids, useful for detecting, preventing, diagnosing, prognosticating, treating and/or amelioratin e.g. gastrointestinal diseases and disorders, or cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAR-2001; 2001US-277340P.
19-JUL-2001; 2001US-306171P.
13-NOV-2001; 2001US-331287P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; secreted protein; digestive disorder; gastrointestinal disorder; mouth; oesophagus; stomach; small intestine; large intestine; liver; bilitary tract; pancreas; cancer; tumour; hyperproliferative disorder; immune disorder; inflammation; infection; wound healing; drug screening;
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antiinflammatory; immunosuppressive; vulnerary; gene thera
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                                                                                                                                                                                                                                                            ABZ71190-ABZ71478 represent cDNAs corresponding to 178 human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                 2003-029900/02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     706 GMTYNDFFMYLTDYDLRVKQYYEVPITMKSVFDLIDTFQSRIKDMEKQKKEGIVCKEDKK 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MVIVYDLIDSMQLRRQEMAIQQSLGMRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                        immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                     disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         secreted protein HSKDA27, SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      950
     and
inflammation, infect and to promote wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΑĀ
                                                                                                                                                                                                                                                                                                 English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                913
                                                                                                                                                                                                                                                                                                                                     treating and/or ameliorating ders, or cancers -
                        infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene therapy.
     healing. Nucleic
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     acids
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RESULT 7
AAB43502
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; antinflammatory; antithyroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coamulant, northermatics
                                                                                                                                                                                                                                                                                                                                                                                                                                               dermatological; neuroprotective; thrombolytic; coagulant; nootropic vasotropic; antipsoriatic; antiangiogenic en therapy; inflammati immune disorder; haematopoietic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the invention may be used for chromosome identification, chromosome mapping, in gene therapy, for identifying individuals from minute biological samples, as hybridisation probes, and as molecular weight markers. The present sequence represents a human secreted protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the invention mapping, in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-FEB-2001
  WPI;
                                                                                                                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                                                                                                                           neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB43502 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                            08-MAR-2000;
                                                                                                                                                                                                                                                                21-SEP-2000.
                                                                                                                                                                                                                                                                                                                     WO200055350-A1
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                                                                                                      (HUMA-) HUMAN GENOME
  2000-587533/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      586
                                              CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121. GMTYNDFFMVLTDVDLRVKQYYEVPITMKSVFDLIDTFQSRIKDMEKQKKEGIVCK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer associated protein sequence SEQ ID NO:947.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LESFCKMATRKISVITIFGPVNNSTMKIDHFQLDNEKPMRVVDDEDLVDQRLISELRKEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MVIVYDLIDSMQLRRQEMAIQQSLGMRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LESFCKMATRKISVITIFGPVNNSTMKIDHFQLDNEKPMRVVDDEDLVDQRLISELRKEY
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                                                    Ruben SM
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                                                                                                                                                                                                                                                                                                                                                                                                                              disease;
                                                                                                                                                                                                            2000WO-US05882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                          99US-0124270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
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81.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                        drug
                                                                                                                                                                                                                                                                                                                                                                                                                           screening
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Pred. No. 8.4e-132;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              950
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                                                                                                                                                                                                                                                                                                            В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cc include: cytostatic; proliferative; vulnerary; immunomodulator; cantidiabetic; antiasthmatic; antixheumatic; antiarthritic; cantinflammator; antithyroid; antiallergic; antibacterial; antiviral; cc antinflammator; antithyroid; antiallergic; antibacterial; antiviral; cc dermatological; neuroprotective; cardiant; thrombolytic; coagulant; cc mootropic; vasotropic; antipsoriatic and antianglogenic. The polymucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. C Polymucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating cor inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune cdisorders, antiergic reactions, graft versus host disease and organ crejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and conditions and antagonists may be also be used in drug screens. AAC7849 to AAC78457 and AAA94240 represent sequences used in the exemplification of the present invention of
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC77607 to AAC78448 encode the human cancer associated proteins gi in AAB43398 to AAB44239. The proteins can have activities based on tissues and cells the genes are expressed in. Example of activities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 1512-1514; 2352pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer - {\sf cancer}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAC77711.
                                                                                                                                                                                                                                                                                                                                                                      Local 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present
                                         235
                                                                             187
                                                                                                                  177
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     247
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                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                     LRKEYGMTYNDFFMVLTDVDLRVKQYYEVPITMKSVFDLIDTFQSRIKDMEKQKKEGIVC
SPMWSMVIVYDLIDSMQLRRQEMAIQQSLGMRC
                                                                                                                                                                                                                               QRDEYLESFCKMATRKISVITIFGPVNNSTMKIDHFQLDNEKPMRVVDDEDLVDQRLISE
                                                                             VGEEVGGVLELFPINGSSVVEREDVPAHLVKDIRNYFQVSPEYFSMLLVGKDGNVKSWYP
                                                                                                                                                        KEDKKQSLENFLSRFRWRRRLLVISAPNDEDWAYSQQLSALSGQACNFGLRHITILKLLG
                                                                                                                                                                                                                                                                                                           QRDEYLESFCKMATRKISVITIFGPVNNSTMKIDHFQLDNEKPMRVVDDEDLVDQRLISE
                                                                                               EEVGGVLELFPINGSSVVEREDVPAHLVKDIRNYFQVSPEYFSMLLVGKDGNVKSWYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                               316 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention.
                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        64.3%;
77.7%;
                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                        Score 1057.5; DB Pred. No. 2e-102;
                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
   279
                                       267
                                                                                                                                                                                                                                                                                                                                                                                                                         DB 21;
                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 316;
                                                                                                                                                                                                                                                                                                                                                                                      61;
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                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                234
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RESULT 8
ABJO5503
ID ABJO
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AC ABJC
XX
DT 14-N
DT Huma
XX
DE Huma
XX
KW Huma
KW gena
XX
COS Homc
COS Homc
CX
PN WO2C
XX
                                               gene
                                                                         Human breast cancer associated polypeptide SEQ ID NO:
                                                                                              14-NOV-2002
                                                                                                                 ABJ05503;
                                                                                                                                   ABJ05503 standard;
                            Homo sapiens
                                              therapy;
                                                        breast
                                                                                             (first
                                              specific gene;
cytostatic.
                                                                                                                                   Protein;
                                                                                            entry)
                                                                                                                                   260
                                                        breast
                                                                                                                                   AA
                                                        specific
                                                        protein;
```

breast

cancer;

WO200264611-A1

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RESULT 9
ABJ18424
ID ABJ18
AC ABJ1
AC ABJ1
XX Cytc
XX Cytc
XX Homc
XX Hom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Вb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Sim:
Matches 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides human breast specific coding sequences proteins. These can be used in the diagnosis and treatment of breast cancer and non-cancerous diseases of the breast. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New breast specific nucleic acids and proteins, useful diagnosing, monitoring, staging, imaging, and treating and non-cancerous disease states in breast tissue, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salceda S,
Sun Y, Liu
                                                                                                                                                                                                                                                                                                                                                        Cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 340-341; 367pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-FEB-2001; 2001US-268292P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-AUG-2002
                              (DIAD-)
                                                                                  22-NOV-2000; 2000US-252509P
                                                                                                                             21-NOV-2001; 2001WO-US43815
                                                                                                                                                                              03-OCT-2002
                                                                                                                                                                                                                                  WO200277232-A2
                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                 metastatic;
                                                                                                                                                                                                                                                                                                                                                                                                      Breast specific related
                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABJ18424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABJ18424 standard; Protein; 260 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (DIAD-) DIADEXUS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2002-657582/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KKGGKTEQDGYQKPTNKHFTQSPKKSVADLLGSFEGKRRLLLITAPKAENNMYVQQRDEY
                                 DIADEXUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVLELF 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GMTYNDFFMVLTDVDLRVKQYYEVPITMKSVFDLIDTFQSRIKDMEKQKKEGIVCKEDKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GMTYNDFFMYLTDVDLRVKQYYEVPITMKSVFDLIDTFQSRIKDMEKQKKEGIVCKEEVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LESFCKMATRKISVITIFGPVNNSTMKIDHFQLDNEKPMRVVDDEDLVDQRLISELRKEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LESFCKMATRKISVITIFGPVNNSTMKIDHFQLDNEKPMRVVDDEDLVDQRLISELRKEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KKGGKTEQDGYQKPTNXHFTQSPKKSVADLLGSFEGKRRLLLITAPKAENNMYVQQRDEY
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C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                 breast
                                                                                                                                                                                                                                                                                                                                                          BSP-agonist; BSP-antagonist; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2002WO-US04197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223
                                                                                                                                                                                                                                                                                                                                 cancer; breast specific; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56.0%;
96.8%;
                                                                                                                                                                                                                                                                                                                                                                                                      amino acid sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hu P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 921; DB 23; Pred. No. 3.4e-88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recipon H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Karra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                     gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cafferkey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for identifying, breast cancer in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
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RESULT 10
AAR90544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
Query Match
Best Local S
Matches 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a novel isolated nucleic acid molecule comprising: a sequence encoding a sequence comprising 11-1518 amino acids; a sequence comprising 190-8144 bp; or a sequence that selectively hybridises to, or having at least 60% identity with the 11-1518 amino acid or 190-8144 nt sequence. The polypeptide and the nucleic acid are useful for treating breast cancer, and diagnosing or monitoring the presence of metastases of breast cancer in a patient. The polypucleotides of the invention can be used to treat disorders by gene therapy. This sequence represents a breast specific related polypeptide of the
                                                                                                                                                                                                Cell cycle; CDK4; regulation; Gl phase; proliferation; tumouriyeme cyclin dependent kinase; differentiation; CDK4 inhibitor; agonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Page 352-353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid molecule, and diagnosing or monitoring the pro
                                                                                             02-JUN-1995;
                                                                                                                                                                 Synthetic.
                                                                                                                                                                                          antagonist
                                                                                                                                                                                                                                         pJG4-5-CDK-BP clone #125 derived
                                                                                                                                                                                                                                                                 08-AUG-1996
                                                                                                                                                                                                                                                                                       AAR90544;
                                                                                                                                                                                                                                                                                                              AAR90544 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salceda S,
                                                                     02-JUN-1994;
                                                                                                                   14-DEC-1995
                                                                                                                                           WO9533819-A2
                                             (MITO-) MITOTIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2003-018927/01.
                                                                                                                                                                                                                                                                                                                                                                           218 QSLENF
                                                                                                                                                                                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                                                                                                         158
                                                                                                                                                                                                                                                                                                                                                                                                                                       121 GMTYNDFFMVLTDVDLRVKQYYEVPITMKSVFDLIDTFQSRIKDMEKQKKEGIVCKEEVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38 KKGGKTEQDGYQKPTNKHFTQSPKKSVADLLGSFEGKRRLLLITAPKAENNMYVQQRDEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KKGGKTEQDGYQKPTNKHFTQSPKKSVADLLGSFEGKRRLLLITAPKAENNMYVQQRDEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                         GMTYNDFFMYLTDYDLRVKQYYEVPITMKSVFDLIDTFQSRIKDMEKQKKEGIVCKEDKK 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΑA;
                                                                     94US-0253155
                                                                                             95WO-US07113
                                                                                                                                                                                                                                                                                                                                                                            223
                                                                                                                                                                                                                                                                                                                                                                                                 186
                                                                                                                                                                                                                 regulation; G1 phase; proliferation; tumourigenesis;
                                                                                                                                                                                                                                                                                                              protein;
                                                                                                                                                                                                                                                                 entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56.0%;
96.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       377pp; English.
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                                                                                                                                                                                                                                                                                                                 278
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Pred. No. 3.4e-88;
1; Mismatches 5
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                                                                                                                                                                                                                                         CDK4 binding protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            260;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
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WPI; 1996-040227/04.

Draetta G,

Gyuris J;

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RESULT 11
AAY60344
ID AAY60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR90533-R90556 are cyclin dependent kinase 4 (CDK4) binding proteins. encoded by clones of the plasmid pJG4-5-CDKBP. CDK4 binding proteins (CDK4-BP) may be used in an assay for screening test compounds as inhibitors of CDK/CDK4-BP interaction. The complexes formed by CDK4 and D-type cyclins are strongly implicated in the control of the early cliphase of the cell cycle and are strong candidates for controlling and/or preventing tumourigenesis and the onset of cancer. Nucleic acids encoding CDK4-BP or fragments of these may be used as probes/primers to diagnose the presence or absence of genetic lesions in a gene encoding 1 of the 24 CDK4-BP, and hence to diagnose the risk for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoding 1 of the 24 CDK4-BP, and hence to diagnose the risk for a subject of developing a cell-proliferation associated disorder (e.g.
                                                                                                                                                                                             Human; bladder; treat
cancer; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cyclin-dependent kinase-4 binding protein (ant)agonists of cell cycle regulation.
  Rosenthal A,
                                                                                                               28-OCT-1999
                                                                                                                                         DE19818620-A1
                                                                                                                                                                                                                                      Human normal bladder tissue EST encoded protein 16
                                                                                                                                                                                                                                                                   31-JAN-2000
                                                                                                                                                                                                                                                                                               AAY60344;
                                                                                                                                                                                                                                                                                                                          AAY60344 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                       21-APR-1998;
                                                                                   21-APR-1998;
                                                                                                                                                                  Homo sapiens
                           (META-) METAGEN GES GENOMFORSCHUNG MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                               249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YLESFCKMATRKISVITIFGPVNNSTMKIDHFQLDNEKPMRVVDDEDLVDQRLISELRKE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KKGGKTEQDGYQKPTNKHFTQSPKKSVADLLG-SFEGKRRLLLITAPKAENNMYVQQRDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 81-82; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                            VGGVLELFPINGSSVVEREDVPAHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                      KQSLENFLSRFRWRRRLLVISAPNDEDWAYSQQLSALSGQACNFGLRHITILKLLGVGEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YGMTYNDFFMVLTDVDLRVKQYYEVPITMKSVLDLIDTFQSRIKDMEKQKKEGIVCKEDK 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KKGGKTEQDGYQKPTNKHFTQSPKEVSGRPAGVLWKANEGLLLITAPKAEE----QQRDE
                                                                                                                                                                                                                                                                                                                                                                                               VGGVLELFPINGSSVVEREDVPAHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YGMTYNDFFMVLTDVDLRVKQYYEVPITMKSVFDLIDTFQSRIKDMEKQKKEGIVCK--- 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YLESFCKMATRKISVITIFGPVNNSTMKIDHFQLDNEKPMRVVDDEDLVDQRLISELRKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         278 AA;
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                                                                                                                                                                                                                                                                  (first entry)
Specht T,
                                                       98DE-1018620
                                                                                   98DE-1018620
                                                                                                                                                                                                           treatment;
                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.9%;
 Hinzmann B,
                                                                                                                                                                                                          EST; expressed sequence tag; cytostatic;
                                                                                                                                                                                                                                                                                                                          783
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Pred.
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                                                                                                                                                                                                                                                                                                                          A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           871; DB 17;
No. 6.8e-83;
                                                                                                                                                                                                                                                                                                                                                                                               273
Schmitt A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              used
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Dahl
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QΥ
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AAB63253
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                  RESULT 12
                                                                                                                                                                                                                                                                                            Matches 168;
                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes novel polypeptide fragment sequences (I) and their encoding nucleic acids (II) which are highly expressed in normal bladder tissue and have cytostatic activity. (II) are used for recombinant expression of (I) and to isolate complete genes. (I) are used to identify agents suitable for the treatment of bladder tumours, to directly treat this form of cancer (including expression from gene therapy vectors), or are used in a preparation for cancer treatment. (I) is also used for the generation of specific antibodies. (II) are identified by assembling ESTs (expressed sequence tags) from a particular tissue type before comparison of expression patterns. This allows a significantly longer fragment of the gene to be revealed, and therefore reduces the number of failures because of ESTs from different intersice.
                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polypeptides and their nucleic acids, useful bladder tumour and identification of therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-602416/52
N-PSDB; AAZ42150.
                                                                                                                                                                                                                                                                                                                                                                                                                                    libraries representing different parts of the same unknown gene distorting the estimated frequency of occurrence in a particular tissue hax(0329-Y60591 represent protein fragments encoded by the human normal
                                                                                                                                                                                                                                                                                                                                                                                                    AAZ42122-Z42248.
                                                                                                                                                                                                                                                                                                                                                                                                                       bladder tissue cDNA library derived EST fragments represented in
                                                                                                                                                                                                                                                                                                             Local
                                                                    664
                                                                                                                                                                                                                    604 KKGGKTEQDGYQKPTNKHFTQSPKKSVADLLGSFEGKRRLLLITAPKAENNMYVQQRDEY
                                                                                                                                                                 61 LESFCKMATRKISVITIFGPVNNSTMKIDHFQLDNEKPMRVVDDEDLVDQRLISELRKEY
                                                                                                                                                                                                                                       1 KKGGKTEQDGYQKPTNKHFTQSPKKSVADLLGSFEGKRRLLLITAPKAENNMYVQQRDEY
                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                               LESFCKMATRKISVITIFGPVNNSTMKIDHFQLDNEKPMRVVDDEDLVDQRLISELRKEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 254; 366pp; German.
                                                                                                                                                                                                                                                                                                                                                                  783
                                                                                                                                                                                                                                                                                            Conservative
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A
                                                                                                                                                                                                                                                                                                             52.8%;
98.8%;
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Pred.
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No. 5.
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.4e-82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for cancer treatment. (I)
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Obata
                             28-MAY-1999;
10-SEP-1999;
                                                                                                                                                                        AAB63253
              (LUDW-) LUDWIG
                                                     26-MAY-2000;
                                                                   07-DEC-2000
                                                                                   WO200073801-A2
                                                                                                  Homo sapiens
                                                                                                                  cancer associated
                                                                                                                         Human;
                                                                                                                                         Human
                                                                                                                                                         26-MAR-2001
                                                                                                                                                                                       AAB63253 standard;
                                                                                                                                        breast cancer associated antigen protein
                                                                                                                        breast cancer; gastric cancer; prostate cancer; diagnosis;
                                                                                                                                                        (first
                                                     2000WO-US14749
              INST CANCER RES
                             99US-0136526.
99US-0153454.
                                                                                                                 antigen; cytostatic;
                                                                                                                                                                                       Protein;
                                                                                                                                                       entry)
                                                                                                                                                                                       188
                                                                                                                                                                                       A
                                                                                                                  cancer vaccine
                                                                                                                                        sequence SEQ
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RESULT 13
ABB03204
ID ABB03
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31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively. AAB6322 to AAB63467, AAB63468 to AAB63721 and AAB6372 to AAB63970 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g. cancer -
                                                                                                                                                                                                                                                                                                                                                                   Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticorvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB03204 standard;
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                                                                                                                                                                                                                                                       WO200155367-A1
                                                                                                                                                                                                                                                                                                                                   musculoskeletal system.
                                                                                                                                                                                                                                                                                                                                                   cardiant; gene therapy; cancer;
neurological disease; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human musculoskeletal system related polypeptide SEQ ID NO 1151.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKGGKTEQDGYQKPTNKHFTQSPKKSVADLLGSFEGKRRLLLITAPKAENNMYVQQRDEY
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2000US-0179065.
2000US-0180628.
2000US-0184664.
2000US-0186350.
2000US-0189874.
2000US-0199874.
2000US-0199123.
2000US-0198123.
2000US-0205515.
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                                                                                                                                                                             2001WO-US01338
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100.0%;
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Pred. No. 4.2e-70;
Pred. No. 4.2e-70;
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12-SEP-2000;
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22-AUG-2000
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22-AUG-2000
23-AUG-2000
30-AUG-2000
01-SEP-2000
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2000US-0236370.
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2000US-0237038.
2000US-0237039.
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2000US-0233065.
2000US-0234223.
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2000US-0218290.
2000US-0220963.
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2000US-0216647.
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2000US-0239937.
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2000US-0236367
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17-NOV-2000;
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20-0CT
20-0CT
20-0CT
The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by
                                                                                                                                                                                                                                                                                                                                                                                                                                  17-NOV-2000;
17-NOV-2000;
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80
                                       Claim 11;
                                                                 Isolated polypeptide for treating, preventing and/or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g.
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17-NOV-2000;
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                                                                                                       2001-451937/48.
DB; AAL34786.
                                     SEQ ID NO 1151; 781pp + Sequence Listing; English
                                                                                                                                                                      2000US-0241787
2000US-0241808
2000US-0241808
2000US-0244807
2000US-0246475
2000US-0246476
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2000US-0246523
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2000US-0246610
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2000US-0246611
2000US-0246611
2000US-0249211
2000US-02511650
2000US-02511858
2000US-02511868
2000US-02511868
2000US-02511899
2000US-02511989
2000US-02511989
2000US-02511989
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                                                                                                                                                      SCI INC
                                                                                                                                    SM;
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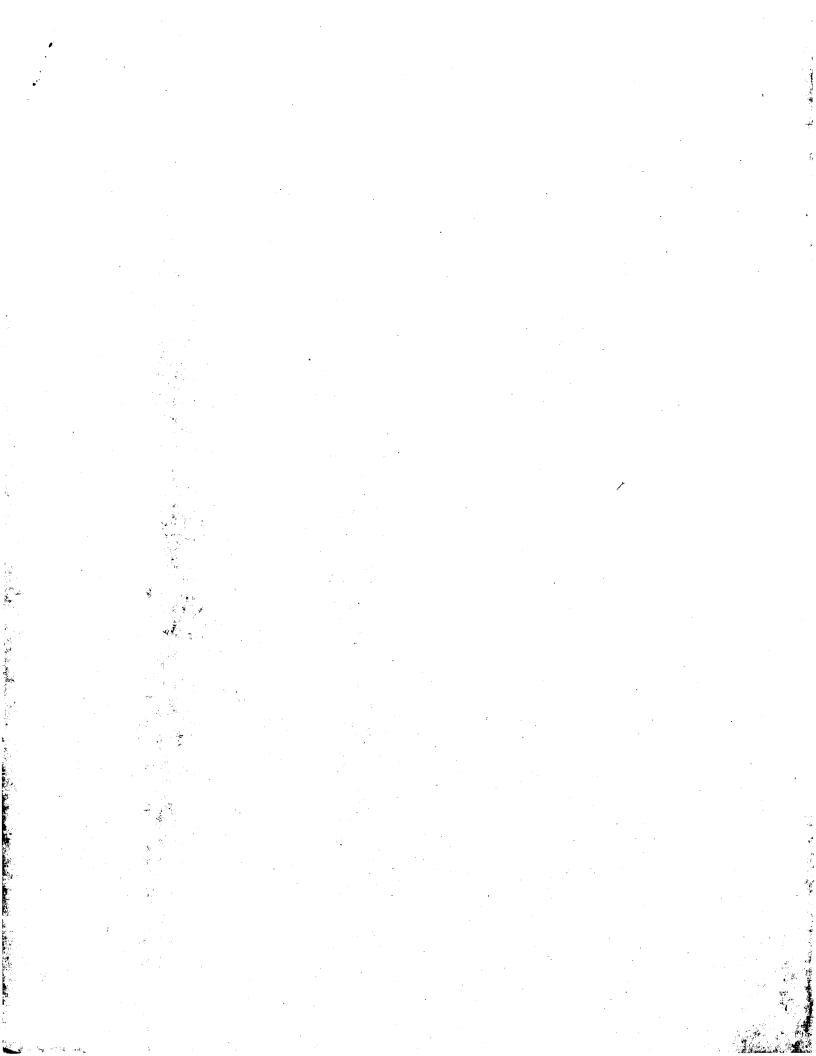
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RESULT 14
ABU12498
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                                                                                  AIDS-related complex; chondrocyte growth; bone regeneration; periodontal regeneration; tissue transport; bone graft; skin aging; keratinocyte growth; hair loss; melanocyte growth; cell proliferation; cell growth; organ transplant; cell differentiation; body height; weight; hair colour; eye colour; skin; percentage of adipose tissue; pigmentation; cosmetic surgery; metabolism; biorhythm; caricadic rhythm; depression; tendency for violence; pain; reproductive capability; hormone level; endocrine level; appetite; libido; memory; stress; storage capability; fat content; lipid content; protein content;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               multiple sclerosis, rheumatoid arthritis and ulcerative colltis; (d) wound (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and
                                                     nutritional
                                                                                                                                                                                                                                                                                                           Musculoskeletal system antigen; cancer; metastasis; re-vascularisation; thrombosis; arteriosclerosis; mineral content;
                                                                                                                                                                                                                                                                                                                                                                                                                                            ABU12498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABU12498 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  parasitic infections.
                                                                                                                                                                                                                                                       post-operative tissue repair; limb regeneration; neuronal growth;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
                                                                                                                                                                                                                                                                                              cardiovascular condition; wound;
                                                                                                                                                                                                                                                                                                                                                                                                        26-FEB-2003
                                                                       carbohydrate
                                                                                                                                                                                                                                                                                                                                                                   Novel human musculoskeletal system antigen #118
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118; Conserv
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                                                   component.
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                                                                       content;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
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                                                                       vitamin content;
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Pred. No. 1.6e
12; Mismatches
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                                                                                                                                                                                                                                                                                            injury; burn; angiogenesis;
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                                                                       cofactor content;
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nes 30;
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Homo sapiens

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02-OCT
02-OCT
 sequence
                Claim 11; SEQ ID NO 1151; 321pp; English
                         Isolated nucleic acid molecules encoding musculoskeletal system associated polypeptides, useful for detecting disorders, e.g. cancer
                                         WPI; 2003-128199/12.
N-PSDB; ABX57774.
                                                                         (ROSE/)
                                                                                                                                                                            29-SEP-2000;
29-SEP-2000;
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05-SEP-2000;
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01-SEP-2000;
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07-JUL-2000;
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                                                          Rosen
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25-SEP-2000;
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                                                                                                                                                                                      29-SEP
                                                                     (BARA/) BARASH S C.
      invention
                                                          CA,
                                                                         ROSEN
RUBEN
ntion describes an isolated nucleic acid molecule comprising encoding musculoskeletal system associated polypeptides use
                                                          Ruben SM,
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                                                                                                              2000US-241809P
2000US-244617P
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Best Local Similarity
Matches 118; Conserv
Secreted protein; human; autoimmune; hyperproliferation; cardiovascular; cerebrovascular; infection; food.
                                                                                                                                                                                                      Sequence
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marrow cells when used in combination with other cytokines; maintains organs before transplantation or for supporting cell culture of primary tissues; induces tissue of mesodermal origin to differentiate in early embryos; increases or decreases the differentiation or proliferation of embryonic stem cells, besides, haematopoietic lineage; modulates mammalian characteristics, such as, body height, weight, hair colour, eye colour, skin, percentage of adipose tissue, pigmentation, size, and shape (e.g., cosmetic surgery); modulates mammalian metabolism; changes mammal's metal state or physical state by influencing biorhythms, caricadic rhythms, depression, tendency for violence, tolerance for pain, reproductive capabilities, hormonal or endocrine levels, appetite, libido, memory, or stress; increases or decreases storage capabilities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for detecting disorders, e.g., cancer or cancer metastases, in animals or humans. The nucleic acid: stimulates re-vascularisation of ischaemic tissues associated with conditions such as thrombosis, arteriosclerosis, and other cardiovascular conditions; treats wounds due to injuries, and other cardiovascular conditions; treats wounds due to injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transports or bone grafts; prevents skin aging due to sunburn by stimulating keratinocyte growth; prevents half loss, since FGF family members activate hair-forming cells and promotes melanocyte growth; stimulates growth and differentiation of hematopoietic cells and bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AIDS-related complex; stimulates chondrocyte growth, thus they can used to enhance bone and periodontal regeneration and aid in tissue
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Gene #12 associated peptide #1.
                                                                               24-APR-2001 (first entry)
                                                                                                                                                                                                                                                 AAB80430 standard; peptide; 505 AA
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.seqdata.uspto.gov/sequence.html?DocID=20020147140
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Pred. No. 1.6e-45;
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Best Local Similarity
Matches 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to 29 human secreted proteins. The invention is used to prevent autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative discorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g. cerebral ischemia, angiogenesis, caused by bacteria, viruses and fungi and ocular disorders e.g. cardiac and infections.
                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 71; 601pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid encoding 29 secreted proteins, for diagnosing, preventing and treating e.g. autoimmune, hyperproliferative, cardiovascular, and ocular diseases or disorders and microorganism infections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosen CA, Ruben SM,
Shi Y, Lafleur DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                 240 VEERYPYPVRLEAMYEVID--QGPIRRIEKIRQKGFVQKCKASGV-----EGQVVAEGN 291
                                                                                                                                                                          133 SSPNILASFAGKNRVWVISAPHASEGYYRLMMSLLKDDVY----CELAERHIQQIVLFHQ 188
                                                                                                                                  138 VKQYYEVPITMKSVFDLIDTFQSRIKDMEKQKKEGIVCKEEVGGVLELFPINGSSVVERE 197
                                                          292 D 292
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                                                                                                                                                                                                                                                            26 SVADLLGSFEGKRRLLLITAPKAENNMY-----VQQRDEYLESFCKMATRKISVITIFGP 80
                                                                                                                                                                                                                                                                                                                                                            505 AA;
                                                                                                                                                                                                                                                                                                9.7%; Score 159.5; DB 22; Length ilarity 29.3%; Pred. No. 1.3e-07; Conservative 35; Mismatches 64; Indels
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Birse CE,
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                                                                                                                                                                                                                                                                                                                            Length 505;
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Title:
Perfect score:
Sequence:
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Maximum DB :
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Run on:
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      10
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                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
     798.5
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seq length: 2000000000
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel!
9: sp_phage:*
                                                                                                                                                                                                         Query
Match
   100.0
61.7
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Gapop 10.0 , Gapext 0.5
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1294
1 KNFFLTNRARERSD
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sp_bacteria:*
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sp_plant:*
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3 Q9YIC1
1 Q8C2J1
3 Q42133
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Q9N0V6
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. Q64698
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Q9XSJ1
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Q99191 macaca fasc
Q99191 macaca fasc
Q99161 coturnix co
Q86291 mus musculu
Q4213 gallus gall
Q91892 brachydanio
Q9n046 bos taurus
Q9192 macaca fasc
Q8uw96 xenopus lae
Q94312 sus scrofa
Q8u415 homo sapien
Q84698 rattus norv
Q9xsj1 ooryctolagus
Q9xsj3 oryctolagus
Q9xsj1 ooryctolagus
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ALIGNMENTS

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Query Best Match		RESULT
	O9GLG1 O9GLG1; O1-MAR-20 O	1 <u>5</u> .
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Quail calpain.
QCAL-1.
QCAL-1.
COturnix coturnix (Common quail).
Pukaryota; Metazoa; Chordata; Crani
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InterPro; IPR002048; EF-hand.
InterPro; IPR001300; Protease_C2.
InterPro; IPR001300; Protease_C2.
InterPro; IPR00169; Shprot_acsite.
Pfam; PF00167; Calpain_III; 1.
Pfam; PF00036; efhand; 2.
Pfam; PF00648; Peptidase_C2; 1.
PRINTS; PR00704; CALPAIN.
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SMART; SM00720; CysPc; 1.

PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.

PROSITE; PS00018; EF_HAND; 1.

PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.

SEQUENCE 705 AA; 80188 MW; 5C70634EB3AA93CD CRC64;
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TISSUE-Skeletal muscle;
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01-MAR-2003
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23,
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61; Mismatches
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; Galliformes; Phasianidae; Phasianinae;
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042133;
042133;
01-JAN-1998 (TrEMBLrel. 05, Cr
01-JAN-1998 (TrEMBLrel. 25, La
01-MAR-2003 (TrEMBLrel. 23, La
MUCL protein (EC 3.4.22.17).
Gallus gailus (Chicken).
Eukaryota; Metazoa; Chordata;
                                 Archosauria;
Gallus.
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Aves;

Neognathae;

Chordata; Craniata; Vertebrata; Euteleostomi; Neognathae; Galliformes; Phasianidae; Phasiani

Phasianinae;

Last sequence update)
Last annotation update)

PRT;

715

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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                Matches 140;
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Q8C2J1;
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                            The FANTOM Consortium,
the RIKEN Genome Exploration Research
"Analysis of the mouse transcriptome b
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AKOMSE47; BAC40416.1; -.
SEQUENCE 713 AA; 82152 MW; 3E1FCB4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-NOD; TISSUE-Thymus;
MEDLINE-22354683; PubMed-12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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                                                               MAIEAAGFKLNKKLHELIITRYSEPDLAVDFDNFVCCLVRLETMFRFFKLLDTDLDGVVT
                                                                                KALEEAGEKMPCQLHQVIVAREADDQLIIDFDNEVRCLVRLETLEKIFKQLDPENTGTIE 239
                                                                                                                                              SDGFSIETCKIMVDMLDSDGSGKLGLKEFYILWTKIQKYQKIYREIDVDRSGTMNSYEMR 179
                                                                                                                                                                                                                 QAVDDEIEANL-EEFDISEDDIDDGFRRLFAQLAGEDAEISAFELQTILRRVLAKRQDIK 119
                                                                                                                                                                                                                                                               TDGFSLDSCRNMVNLMDKDGSARLGLVEFQILMNKIRSWLTIFRQYDLDKSGTMSSYEMR
FDLFKWL
                             LDLISWL 246
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                                                                                                                                {\tt TNGFSLESCRSMVNLMDRDGNGKLGLVEFNILWNRIRNYLTIFRKFDLDKSGSMSAYEMR}
                                                                                                                                                                                              QELDDQIQANLPDEKVLSEEEIDDNFKTLFSKLAGDDMEISVKELQTILNRIISKHKDLR
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707
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56.7%;
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                                                                                                                                                                                                                                                                                                                              Score 773.5; DB 1
Pred. No. 1.7e-54;
8; Mismatches 48
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Sciurognathi; Muridae;
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based on functional
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annotation
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Best Loc
Matches
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InterPro; IPRO01300; Protease_C2.
InterPro; IPRO0169; Shprot_acsit
Pfam; PF01067; Calpain_III; 1.
Pfam; PF00036; efhand; 3.
Pfam; PF00048; Peptidase_C2; 1.
PRINTS; PR00704; CALPAIN_
SMART; SM00720; Calpain_III; 1.
SMART; SM00230; CysPc; 1.
SMART; SM00230; CysPc; 1.
SMART; SM00018; EF_HAND; 2.
PROSITE; PS00018; EFHAND; 2.
PROSITE; PS00139; THIOL_PROTEASE_
                                            0918G2;
01-0CT-2000 (TrEMBLrel. 15,
01-0CT-2000 (TrEMBLrel. 15,
01-MAR-2003 (TrEMBLrel. 23,
Calpain 1 (EC 3,4.22,17).
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Brachydanio rerio (2ebrafish) (Danio re:
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jeong S.-Y., Sorimachi H., Lee H.-J., Ishiura S., Suzuki "Molecular cloning and characterization of cDNAs for the subunit and the small subunit of chicken calpain."; Comp. Biochem. Physiol. 118B:539-547(1997).
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expresses four of
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MEDLINE=95260862; Pu
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distinct calpains.";
ys. Acta 1261:381-393(1995).
                                                                                                                                                                                                                                         246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EF_HAND; 2.
THIOL_PROTEASE_CYS; 1.
; 81411 MW; 70679B21C5E0AD6A CRC64;
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PubMed=7742367;
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Pred. No. 7.8e
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                  Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 142
                                                                                                                                                                                                                                    Q9N0V6 PRELIMINARY;
Q9N0V6; Q9N0U3;
01-OCT-2000 (TremBLrel. 15, Cr
01-JUN-2002 (TremBLrel. 21, La
01-MAR-2003 (TremBLrel. 23, La
Micromolar calcium activated n
                                                                                                                                              Mammalia; Eutheria; C
Bovidae; Bovinac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; P
PROSITE; P
Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cyprinidae; Danic
NCBI_TaxID=7955;
[1]
J. Anim.
[2]
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART;
SMART;
SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro: IPR002048; EF-hand.
InterPro: IPR001300; Protease_C2.
InterPro: IPR001169; SHprot_acsite.
Pfam; PF01067; Calpain_III; 1.
Pfam; PF00036; efhand; 3.
Pfam; PF00048; Peptidase_C2; 1.
                             MEDLINE=20500419; PubMed=11048924; Smith T.P.L., Casas E., Rexroad C. "Bovine CAPNI maps to a region of trait locus for meat tenderness."; J. Anim. Sci. 78:2589-2594(2000).
                                                                                                                                                                                                        Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00704; CALPAIN.
SMART; SM00720; calpain_III;
SMART; SM00230; CysPc; 1.
SMART; SM00054; EFh; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Zebrafish calpain 1 (canp1) phylogenetic implications."; Submitted (JUN-2000) to the EMBL; AF282675; AAF82808.1;
                                                                                                             SEQUENCE
                                                                                                                                                                                                                          CAPN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lee
                                                                                                                                          NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P04574; 1ALV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             572
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142; Conser
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PS00139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KNFFLTNRARERSDTFINLREVLNRFKLPPGEYILVPSTFEPNKDGDFCIRVFSEKKADY
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FROM
                                                                                                              FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                               LDLISWLCFSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FROM N.A.
Evans C.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   704
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                                                                                                             N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EF_HAND; 2.
THIOL_PROTEASE_CYS;
                                                                                                                                                           Bos.
                                                                                                                                                                        Chordata; Crania
Cetartiodactyla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30090 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                   702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51;
                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
d neutral protease 1.
                                                                                                                                                                                                                                                                                     Created)
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Pred. No. 1.
                                                                                                                                                                                          Craniata;
                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                             III, Kappes
                                                                                                                                                                          Ruminantia;
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                                                             I, Kappes S.M., containing a q
                                                                                                                                                                                         Vertebrata;
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57;

Indels Length

631

571

511 60

704; 1;

Pecora;

Bovoidea;

., Keele J.W.; quantitative

Euteleostomi;

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991N36
11D 185
12D 185
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Best Local
                                                                                    Smith T.P.L., Casas E., Rexroad C.E.,
"Bovine CAPNI maps to a region contal
Submitted (JAN-2000) to the EMBL/GenB
EMBL; AF221129; AAF32364.1; -.
HSSP; PO4574; 1ALV
InterPro; IPR002048; EF-hand.
InterPro; IPR001300; Protease_C2.
InterPro; IPR00169; SHprot_acsite.
Pfam; PF00067; Calpain_III; 1.
Pfam; PF00036; efhand; 3.
Pfam; PF00048; Peptidase_C2; 1.
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01-OCT-2000
01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Cetartioda
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam;
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EMBL; AF252504; AAF
HSSP; P04574; 1ALV.
                         PRINTS; PR00704;
SMART; SM00720; o
SMART; SM00230; o
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Micromolar
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PF00036; efhand; 3.
PF00648; Peptidase_C2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IT.P.
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SM00720; calpain_III; 1.
SM00230; CYSPC; 1.
SE; PS00018; EF_HAND; 2.
SE; PS00139; THIOL_PROTEASE_CYS;
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IPR000169; SHprot_acsite.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                716 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
calcium-dependent neutral protease large
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Casas E.,
                         calpain_III; 1.
CysPc; 1.
                                                                      CALPAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82249 MW;
                                                                                                                                                                                                                                                                      E., Rexroad C.E., Kappes S.M., Keele o a region containing a QTL for meat to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   road C.E. III, Kappes S.M., Keele J.W.; EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 761.5; DB 6; Pred. No. 1.7e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8FFD61331DAB8AD5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    716;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Bovoidea;
                                                                                                                                                                                                                                                                                                  tenderness
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RESULT
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                                         Query Match
Best Local S
Matches 137
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Best Local
                                                                                                                    Pfam; PF01067; Calpain_III; 1.
Pfam; PF00036; efhand; 3.
Pfam; PF00036; efhand; 3.
Pfam; PF00648; Peptidase_C2; 1
PRINTS; PR00704; CALPAIN.
SMART; SM00720; calpain_III; 1
SMART; SM00230; CysPc; 1.
SMART; SM00054; EFh; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00018; FPROSITE; PS00139; Protease: Protease: SEQUENCE 716 AA;
                                                                                                                                                                                                                                                                                                                                                                                                            Q9GLG2;
Q9GLG2;
Q1-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                     PROSITE; PS00018; PROSITE; PS00139; SEQUENCE 714 AA;
                                                                                                                                                                                                                                                      Submitted (JUL-2000) to the EMBL; AF284440; AAG22770.1;
                                                                                                                                                                                                                                                                                                                                                      Macaca fascicularis (Crab eating macaque) (Cynomolgus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheci
                                                                                                                                                                                                                                   MEROPS;
                                                                                                                                                                                                                                                                                       Nakajima T.,
                                                                                                                                                                                                                                                                                                   TISSUE-Retina
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                              Cercopithecinae;
                                                                                                                                                                                                                                                                                                                                                                                         Calpain
                                                                                                                                                                                                 InterPro; IPR001300;
InterPro; IPR000169;
                                                                                                                                                                                                                        InterPro; IPR002048;
                                                                                                                                                                                                                                              HSSP; P04574;
                                                                                                                                                                                                                                                                             "Calpain isoforms in
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462
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                                          al Similarity
137; Conserv
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137; Conser
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           KNFFLTNRARERSDTFINLREVLNRFKLPPGEYILVPSTFEPNKDGDFCIRVFSEKKADY
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                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                      Fukiage C.,
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                                                                                                                                                                                                                                              1ALV.
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                                                                                                                                                                                                                                                                                                                                              Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     710
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                                                                                     EF_HAND; 2.
THIOL_PROTEASE_CYS; 1.
; 81849 MW; 834690C214DE7AD8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EF_HAND; 2.
THIOL_PROTEASE_CYS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82207 MW; A7F55C197BD5DF23 CRC64;
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55.5%;
                                                      58.6%;
55.5%;
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                                                                                                                                                                                                             Protease_
                                                                                                                                                                                                                        EF-hand
                                                                                                                                                                                                                                                                            Azuma M., Shea
eye of monkey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59;
                                           57;
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Last
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                                                                                                                                                                 <u>-</u>
                                         Score 758.5; DB 6;
Pred. No. 2.9e-53;
7; Mismatches 52;
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Pred. No. 1.7e-53
9; Mismatches 5
                                                                                                                                                                                                             _C2
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                                                                                                                                                                                                                                                                                       T.R.;
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                                                               Length
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                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                              monkey).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  716;
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                                          Gaps
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 521
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RESULT DRUW966 TO BUW966 TO BUW96 TO BUW966 TO BUW96 TO BUW966 TO BUW96 TO BUW966 TO BUW96 TO BUW96 TO BUW96 TO BUW96 TO BUW96 TO BUW96 
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
PROSITE;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8UW96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Xenopus has a calpain most similar to mu/m-type chicken Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AB061521; BAB83262.1;
InterPro; IPR001300; Protease_C2.
InterPro; IPR001300; Protease_C2.
InterPro; IPR000169; SHprot_acsite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00720; calpain_III; SMART; SM00230; CysPc; 1. SMART; SM00054; EFh; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Ve
Amphibia; Batrachia; Anura; Mesobatrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mu/m-calpain large subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                    513
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                                       220
                                                                                                                                                                                                                                                                                                                                                           453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF01067; Calpain_III; 1.
PF00036; efhand; 2.
PF00648; Peptidase_C2; 1.
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                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                  142;
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                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00018; EF_HAND; 2.
PS00139; THIOL_PROTEASE_CYS;
724 AA; 81770 MW; CA5CB0
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                                                                                                                                                                                              QAVDDEIEANL-EEFDISEDDIDDGFRRLFAQLAGEDAEISAFELQTILRRVLAKRQDIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246
                                                                                                                                                                                                                                                                                                                                                                                                                                           57.0%; Score 737; D) 52.4%; Pred. No. 1.60 tive 55; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CA5CB090AE7A4288 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 13;
1.6e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vertebrata; Euteleostomi;
ia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA
                                                                                                                                                                                                                                                                                                                                                                                                                                             52;
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                                                                                                                                                                      632
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         RESULT ON A COLOR OF A
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Best Local Sin
Matches 125;
Ol-MAR-2003 (TrEMBLrel. 12, Lans-specific calpain Lp82.
Sus scrofa (Pig).
Eukaryota: Martheology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002048; EF-hand.
InterPro; IPR001300; Protease_C2:
InterPro; IPR00169; SHPOT_acsit
Pfam; PF01067; Calpain_III; 1.
Pfam; PF000548; Peptidase_C2; 1.
PRINTS; PR00704; CALPAIN.
                                                                        Q9XSJ2
Q9XSJ2;
Q1-NOV-1999
Q1-NOV-1999
Q1-MAR-2003.
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Q918T0;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00704; CALPAIN.

SMART; SM00720; calpain_III; 1.

SMART; SM00230; CysPc; 1.

PROSITE; PS00018; EF_HAND; 1.

PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.

SEQUENCE 702 AA; 79466 MW; 6D66A3B1D276DC51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A novel xenopus gene homolo Submitted (JUL-2000) to the EMBL; AF212199; AAF63194.2; HSSP; P04574; 1ALV.
MEROPS; CO2.007; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordati
Amphibia; Batrachia; Anura;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000
01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhao H.,
                                                                                                                                                                                                                                                                                                          DLISWLCFSVL
                                                                                                                                                                                                                                                                                                                                                                                                     ALEEAGFKMPCQLHQVIVARFADDQLIIDFDNFVRCLVRLETLFKLFKQLDPENTGTIEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGFSIETCKIMVDMLDSDGSGKLGLKEFYILWTKIQKYQKIYREIDVDRSGTMNSYEMRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QAVDDEIEANLEEFDISEDDIDDGFRRLFAQLAGEDAEISAFELQTILRRVLAKRQDIKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KNEFLINRARERSDTFINLREVLNRFKLPPGEYILVPSTFEPNKDGDFCIRVFSEKKADY
                                                                                                                                                                                                                                                                                  SLQEWLCATLV 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGFTLNTCREMISLQDMDGTATLSLLEFRILWMKIQKYLAIYLKADSDRSGIMDSHELRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEVGDVVIAKPYEPQISNKDVPDDFKNIFDKLAGDKEEVDARELQTILNKLISKRPDLRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RDFLQKTPTAARSDTYINVREVSNRFHLPVGDYLIVPSTFEPFKNGDFCLRVFSEKEAKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEAMFKFFKALD-EGDGTAEMNLGEWLTMTM 722
                                                                                                                                                                                                                                                                                                                                                                       ALQEAGFTLNNKIHESIVQRYASNDLALNFDGFIACMMRLETLFKMFQMLDKSKRGVVEL
         Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) (TrEMBLrel.) (TrEMBLrel.) (TrEMBLrel.
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                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grunz H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ican clawed
Chordata; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHprot_acsite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protease_C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homologous to rat calpain.";
to the EMBL/GenBank/DDBJ data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15,
23,
                                                                        Last sequence update)
Last annotation update)
                                                                                                                       Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 667; DB 13; Pred. No. 7.7e-46; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d frog).
Craniata;
                                                                                                                                                                    PRT;
         Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                      709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    702
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ia; Pipoidea; Pipidae;
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Best Local S
Matches 117
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InterPro; IPRO01300; Protease_C2.
InterPro; IPRO01300; Protease_C2.
InterPro; IPRO0169; Shprot_acsite.
Pfam; PF00167; Calpain_III; 1.
Pfam; PF000036; efhand; 3.
Pfam; PF000048; PeptLddsse_C2; 1.
PRINTS; PR00704; CALPAIN_
SMART; SM00720; Calpain_III; 1.
SMART; SM00720; CysPc; 1.
SMART; SM00234; EFh; 2.
                                                                                                                                                                                                           Q8N4R5;
01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
PROSITE;
                                                     InterPro;
InterPro;
InterPro;
                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                        Calpain .... Human).
Homo sapiens (Human).
Chordata;
                                                                                                                                                                                                                                                           Q8N4R5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ma H., Shearer T.R.;
Submitted (MAY-1999) to the
EMBL; AF148955; AAD34600.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEROPS; C02.004;
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                                                                                       EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia;
                                                                                                           Strausberg R.;
                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                   Submitted
                                                                                                                         TISSUE=Brain;
                                                                                                                                   SEQUENCE FROM
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                              tted (JUL-2002) to the EMBL/GenBank/DDBJ
BC033733; AAH33733.1; -.
Pro; IPR002048; EF-hand.
Pro; IPR001300; Protease_C2.
Pro; IPR00169; SHprot_acsite.
Pro1067; Calpain_III; 1.
PF00036; efhand; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                            113
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117; Conser
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                       PF00648;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS00018; EF_HAND; 2.
PS00139; THIOL_PROTEASE_CYS;
709 AA; 82591 MW; 3E812B
                                                                                                                                                                                                                                                                                                                                                                                                                                                           KNFFLTNRARERSDTFINLREVLNRFKLPPGEYILVPSTFEPNKDGDFCIRVFSEKKADY
                                                                                                                                                                                                                                                                                                                 DGDGIIKLNVLEWL
                                                                                                                                                                                                                                                                                                                                      ENTGTIELDLISWL
                                                                                                                                                                                                                                                                                                                                                                         MNSYEMRKALEEAGFKMPCQLHQVIVARFADDQLIIDFDNFVRCLVRLETLFKIFKQLDP
                                                                                                                                                                                                                                                                                                                                                                                                      NKHKDLKTEGFTLESCRSMIALMDTDGSGRLNLQEFHHLWKKIKSWQKIFKHYDTDQSGT
                                                                                                                                                                                                                                                                                                                                                                                                                            AKRODIKSDGFSIETCKIMVDMLDSDGSGKLGLKEFYILWTKIQKYQKIYREIDVDRSGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EEVENTISVDRPVPEPSNTDQ----ESEEQQQFRNIFRQIAGDDMEICADELKNVLNRVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KDFFLYNASKARSRTYINMREVSERFRLPPSEYVIVPSTYEPHQEGEFMLRVFSEKRKLS
                                                                                                                                                                                                                                                                                                                                                            INSYEMRNAVNDAGFHLNNQLYDIITMRYADKYMNIDFDSFIRCFVRLEGMFRAFSAFDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                           PRELIMINARY;
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           Peptidase_C2;
; CALPAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                    Primates;
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                                                                                                                                                                                                                                                                                                                 703
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22,
23,
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 648; DB 6;
Pred. No. 2.7e-44;
                                                                                                                                                                    Craniata; V
Catarrhini;
                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3E812BC2C1E9A1F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                           702
                                                                                                                                                                              Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                           B
                                                                                                                                                                     Hominidae;
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                                                                                                   databases
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                                                                                                                                                                     Homo
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RESULT 13
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DR
DR
SQ
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Best Local S
Matches 122
                                                                                                                                                                                                                                                                                                                                                                                                                     Q64698
Q64698;
01-NOV-1996 (TrEMBLrel. 0
01-NOV-1996 (TrEMBLrel. 0
01-MAR-2003 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00720; calpain_III; 1.
SMART; SM00230; CysPe; 1.
SMART; SM00054; EFh; 2.
PROSITE; PS00018; EF_HAND; 2.
PROSITE; PS00019; THIOL_PROTEASE_CYS; 1.
PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Calpain, large (Catalytic) subunit (EC 3.4.22.17) (
neutral proteinase) (CANP) (Stomach-specific calciu
                                                                                                                                                                                                                                                                                                                                                                           protease large subunit) (NCL2).
CLS4.
               <del>: : :</del>
                                                                                                                                                                                                               without Ca(2+)-binding domain.";
J. Biol. Chem. 268:19476-19482(1993)
                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae
                                                                                                                                                                                                                                  Sorimachi H., Ishiura S., Suzuki K.;
"A novel tissue-specific calpain species expressed predominantly
the stomach comprises two alternative splicing products with and
                                                                                                                                                                                                                                                                                        TISSUE-STOMACH
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus
                                                                                                                                                                        -!- SUBUNIT: HETERODIMER OF A LARGE (CATALYTIC)
                                                                                                                                                                                                   -! - FUNCTION:
                                                                                                                                                                                                                                                                           MEDLINE=93374936; PubMed=7690035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hes 122;
                                                                                                                                                                                      PROTEASES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QAVDD-EIEANLEEFDISEDDIDDGFRRLFAQLAGEDAEISAFELQTILRRVLAKRQDIK 119 :|: | : | : | : | : | : | : | : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KNFFLTNRARERSDTFINLREVLNRFKLPPGEYILVPSTFEPNKDGDFCIRVFSEKKADY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSLEQWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KALEEAGFKMPCQLHQVIVARFADDQLIIDFDNFVRCLVRLETLFKIFKQLDPENTGTIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TKGFGLDACRCMINLMDKDGSGKLGLLEFKILWKKLKKWMDIFRECDQDHSGTLNSYEMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEFFTKYQDHGFSEIFTNSREVSSQLRLPPGEYIIIPSTFEPHRDADFLLRVFTEKHSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                   CALPAINS
                                                                                                                                                                                                                                                                                                   N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    696
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                                                                                                                                                                                                                                                                                                                                                              (Rat).
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                                                                                                                                                                                                   ARE CALCIUM-ACTIVATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50;
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Pred. No. 3.6e
50; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        703
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                                                                                                                                       (SHOWN HERE) AND NCL2'; ARE
                                                                                                                                                                                                                                                                                                                                      Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74;
                                                                                                                                                                                                   NON-LYSOSOMAL
                                                                                                                                                                                                                                                                                                                                                                                                  calcium-activated neutral
                                                                                                                                                                           AND
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                                                                                                                                                                                                                                                                                                                                                                                                              (Calcium-activated
                                                                                                                                                                            A SMALL
                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
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                                                                 FORMS
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O9XSJ3

C 09XSJ3;

T 01-NOV-1999 (TrEMBLrel. 12, Created)

T 01-NOV-1999 (TrEMBLrel. 12, Last sequence updat

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation upc

E Lens-specific calpain Lp82.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertek

CC Eukaryota; Metazoa; Lagomorpha; Leporidae; Or
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InterPro; IPR00169; Shprot_acsite.
Pfam; PP01067; Calpain_III; 1.
Pfam; PF00036; efhand; 4.
Pfam; PF00648; Peptidase_C2; 1.
PR.NTS; PR00704; CALPAIN.
SMART; SM00720; calpain_III; 1.
SMART; SM00230; CysPc; 1.
SMART; SM00054; EFh; 2.
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D14479;
D14480;
P04574;
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                                                                                                                                                                                                                                RDFFLGRQPSTCSSTYMNLREVSSRVRLPPGQYLVVPSTFEPFKDGDFCLRVFSEKKAKA
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BAA03370.
BAA03371.
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48.4%;
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II, THIOL PROTEASE.
III.
IV, CALCIUM-BINDING.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
SITE I (PROBABLE).
SITE II (PROBABLE).
SITE II (PROBABLE).
ANCESTRAL CALCIUM SITE IV (POTENTIAL).
ANCESTRAL CALCIUM SITE IV (POTENTIAL).
G -> V (IN ISOFORM NCL2').
T -> S (IN ISOFORM NCL2').
MISSING (IN ISOFORM NCL2').
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Pred. No. 4.1e-43;
4; Mismatches 70;
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                       Vertebrata; Euteleostomi;
                                                        update)
                Oryctolagus
                                               update)
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[1]
SEQUENCE FROM N..

Ma H., Shearer T.R.;

Ma H., Shearer T.R.;

Submitted (MAY-1999) to the
InterPro; IPRO02048; EF-hand.

DR InterPro; IPRO01300; Protease_C2.

InterPro; IPRO00169; SHprot_acsite.

Pfam; PF00036; efhand; 3.

DR Pfam; PF00036; efhand; 3.

PRINTS; PR00704; CALPAIN.

"SM00720; calpain_III; 1.

"SM00720; calpain_III; 1.
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Best Local S
Matches 114
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InterPro; IPR001300; Protease_C2.
InterPro; IPR001300; Protease_C2.
InterPro; IPR00169; Selpot_acsite.
Pfam; PF01067; Calpain_III; 1.
Pfam; PF00036; efhand; 3.
Pfam; PF000648; Peptidase_C2; 1.
PRINTS; PR00704; CALPAIN.
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Q9XSJ1;
Q1-NOV-1999 (TrEMBLrel. 12, CO1-NOV-1999 (TrEMBLrel. 12, LO1-NOV-1999 (TrEMBLrel. 23, Lens-specific calpain Lp82.
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SMART; SM00720; calpain_III;
SMART; SM00230; CysPc; 1.
SMART; SM00054; EFh; 2.
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Submitted (MAY-1999) to the
EMBL; AF148956; AAD34601.1;
HSSP; P04574; IALV.
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PROSITE; PS00139; THIOL_PROTEASE_CYS;
SEQUENCE 709 AA; 82559 MW; B5FB1C
                                                                                                                                                                                                                                                                                           Bovidae; Bovinae;
NCBI_TaxID=9913;
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Mammalia; Eutheria;
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Last sequence update)
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Search completed: July 24, 2003, 12:56:54
Job time : 34.0498 secs
                                                                                                                                                                                                                                       Query Match 48.8%; Score 631; DB 6; Length 709; Best Local Similarity 46.4%; Pred. No. 6.6e-43; Matches 116; Conservative 65; Mismatches 65; Indels
                                                                                                                                                                                                                                                                             SEQUENCE 709 AA; 82634 MW; 213150151408CC50 CRC64;
                                                                             694 IIKLNVLEWL 703
                                                  237 TIELDLISWL 246
                                                                                                                                                          574 DLKTQGFTLESCRSMIALMDTDGSGRLNLQEFHHLWKKIKTWQKIFKHYDTDQSGTINSY
                                                                                                                              4.
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Title:
Perfect score:
Sequence:
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    Searched:
                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                     July 24, 2003, 12:28:44 ; Search time 6.93849 Seconds (without alignments) 1701.191 Million cell updates/sec
127863 seqs, 47026705 residues
                                                                                             US-09-884-319A-6
1294
1 KNFFLTNRARERSDTFINLR......PENTGTIELDLISWLCFSVL 251
                                                                                                                                                                                                                                                                                                               GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

127863

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1122 1122 1122 1122 1122 1122 1122 112	Score
1235 1235 1235 1235 1235 1230 1210 1210 1210 1210 1210 1210 1210	
9959 9959 9959 9959 9959 9959 9959 995	Query Match I
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	Description
homo sapien sus scrofa oryctolagus mus musculu rattus norv gallus gallus gallus gallus gallus gallus gallus sarota homo sapien sus scrofa homo sapien gallus gallus gallus sus scrofa lomo sapien sus scrofa oryctolagus homo sapien sus scrofa oryctolagus scrofa oryctolagus sus scrofa oryctolagus sus scrofa oryctolagus sus scrofa oryctolagus sus scrofa oryctolagus mus musculu homo sapien rattus norv drosophila schistosoma homo sapien cricetulus scrofa schistosoma homo sapien sus scrofa schistosoma scrofa schistosoma scrofa schistosoma scrofa schistosoma caenorhabdi mus musculu	-

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640	148	532 640	640 147	95 169	191 335
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CAN5_HUMAN	CALM_CAPAN CALM_PNECA	CDPK_DAUCA	CAN5_MOUSE CALM_FAGSY	CATR_CHLRE	PCD6_HUMAN YG25_YEAST
	P93087 capsicum an P41041 pneumocysti				

ALIGNMENTS

DRANDARD; PRI ORWU26; O9HBB1; 1. 15, Created) 1. 15, Created) 1. 15, Last sequen 1. 42, Last annote bed neutral prote; pain) (Calpain lai zona; Chordata; Cra ria; Primates; Cai 4, PubMed=2852952 4, Ohno S., Emoi hip of the cDNA for fing form of human 2012-8128(1988). 2012-8128(cDNA sequences." d. Sci. U.S.A. 99	R R	
NAN_HUMAN STANDARD; OPHBBL; 17655; 016738; 08WUZ6; OPHBBL; 17406-1990 (Rel. 15, Created) 1 AUG-1990 (Rel. 15, Created) 1 AUG-1990 (Rel. 15, Last sequence update) 5 SEP-2003 (Rel. 42, Last annotation update) 1 Sep-2003 (Rel. 42, Last annotation update) 2 large [catalytic] subunit precursor (EC 3.4.22.17) 2 alcium-activated neutral proteinase) (CANP) (M'type) (M'calpai) 2 lipting (Human). 2 mo sapiens (Human). 2 mo sapiens (Human). 2 mo sapiens (Human). 3 mo sapiens (Human). 3 mo sapiens (Human). 3 mo sapiens (Human). 4 majoh S., Aoki K., Ohno S., Emori Y., Kawasaki H., Sugihara H., 1 majoh S., Aoki K., Ohno S., Emori Y., Kawasaki H., Sugihara H., 1 majoh S., Aoki K., Ohno S., Emori Y., Kawasaki H., Sugihara H., 1 majoh S., Aoki K., Ohno S., Emori Y., Kawasaki H., Sugihara H., 2 mo sapiens (Human) 4 clecular cloning of the cDNA for the large subunit of the 2 specific orm of human Ca2+-activated neutral proteases 2 connor J.R.; 3 pubMed-10944468; 3 L., Connor J.R.; 5 pubMed-10944468; 5 L., Connor J.R.; 5 pubMed-10944468; 6 L., Connor J.R.; 5 pubMed-10944468; 6 L., Connor J.R.; 5 pubMed-10944468; 7 pubMed-10944468; 8 pubMed-10944468; 8 pubMed-10944468; 8 pubMed-10944468; 9 pubMed-1094468; 9 pubMed-10944468; 9 pubMed-1094468; 9 pubMed-10944468; 9 pubMe	u11-	RA	
MAN_HUMAN STANDARD; OPHBBL; 17655; O16738; O8WUZ6; O9HBBL; 176051990 (Rel. 15, Created) 17805-1990 (Rel. 15, Last sequence update) 17805-1990 (Rel. 16, Last sequence update) 17805-1990 (Rel. 17, Last sequence update) 17805-1990 (Rel. 18, Last sequence update) 17806-1990 (Rel. 19, Last sequence update) 17807-1990 (Rel. 19, Last sequence update) 18908-1990 (Rel. 1990 (Rel. 1990) 18908-1990 (Rel. 1990 (Rel. 1990) 18908-1990 (Rel. 1990) 19908-1990 (Rel. 1990) 19908-19908-1990 (Rel. 1990) 19908-	Su	RA	
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NAN_HMMAN STANDARD; PRT; 700 AA. 17655. Q16738; Q8WU26; Q9HBB1; 1-AUG-1990 (Rel. 15, Created) 1-AUG-1990 (Rel. 15, Created) 1-AUG-1990 (Rel. 15, Last sequence update) 1-AUG-190 (Rel. 16, Last sequence update)	Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanche	RA A	
NAN_HUMAN STANDARD; PRT; 700 AA. NAN_HUMAN Rel. 15, Created) 1-AUG-1990 (Rel. 15, Last sequence update) 1-AUG-1990 (Rel. 16, Last sequence update) 1-AUG-1990 (M-Calpain update)	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk	RA.	
NAN_HOWAN STANDARD; PRT; 700 AA. 17655; 016738; 08WU26; 09HBB1; 1-AUG-1990 (Rel. 15, Created) 5-SEP-2003 (Rel. 42, Last sequence update) 5-SEP-2003 (Rel. 42, Last annotation update) 1-AUG-1990 (Rel. 15, Last sequence update) 1-AUG-1990 (Rel. 15, Last sequence update) 1-AUG-1990 (Rel. 42, Last annotation update) 1-AUG-1990 (Rel. 15, Last sequence update) 1-AUG-1990 (Rel. 16, Last sequence update) 1-	S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.A., McEwan P.T., McKernan K.J., Malek J.A., Gunaratne P	R R A	
JMAN JMAN STANDARD; PRT; 700 AA. 17655; 016738; 08WU26; 09HBB1; 1-AUG-1990 (Rel. 15, Created) -SEP-2003 (Rel. 42, Last sequence update) -SEP-2003 (Rel. 42, Last annotation update) -Alcium-activated neutral proteinase) (CANP) (M-type) -Alliumolar-calpain) (Calpain large polypeptide L2). NOT OR CANPL2 JMAN MARYOTE METAZOA; Chordata; Craniata; Vertebrata; Eutammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho -BI_TaxID=9606; BULINE-89166474; PubMed-2852952; BOLINE-89166474; PubMed-2852952; MAJOH S., Aoki K., Ohno S., Emori Y., Kawasaki H., Suguzuki K.; SOUENCE FROM N.A. 15SUE-Astrocytoma; DULINE-20403900; PubMed-10944468; 2. Connor J.R.; DLINE-20403900; PubMed-10944468; 2. Connor J.R.; DLINE-20403900; PubMed-10944468; 2. Connor J.R.; SOUENCE FROM N.A. ISSUE-Astrocytoma; SOUENCE FROM N.A. ISSUE-Pancreas; ESUE-Pancreas; ESUIE-Pancreas; EDLINE-2038857; PubMed-12477932; EDLINE-2038857; PubMed-12477932; EDLINE-2038857; PubMed-12477932; ELIGNUE R.D., Collins F.S., Wagner L., Shenemen C.M., Shenemen C.M., Scareard T., Marusina K., Farmer A.A., Rubin G.M., Labelton M.F., Casavant T., Lebelton M. S., Soareafer C.F., Shenefer C.F., Shenefer C.F., Jordan H., Moore T., Max S.I., Wang J., Hatchenho L., Marusina K., Farmer A.A., Rubin G.M., I., Lebelton M. S., Soareafer C.F., Shenefer	., Carninci P., Prange	RA	
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CAN2_HUMAN	AN2_HUMAN STANDARD; PRT; 700	S II	
	HUMAN	CAN2_	

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DR MIM; 114230; -.

DR GO; GO:0008234; F:cysteine-type peptidase activity; TAS.

DR Interpro; IPR002048; EF-hand.

DR Interpro; IPR001300; Protease_C2.

DR Interpro; IPR00169; SHprot_acsite.

DR Pfam; PF00067; Calpain_III; 1.

DR Pfam; PF00036; efhand; 3.

DR Pfam; PF00036; calpain_III; 1.

DR Pfam; PF000704; CALPAIN_III; 1.

DR SMART; SM00720; calpain_III; 1.

DR SMART; SM00720; Calpain_III; 1.

DR SMART; SM00720; Calpain_III; 1.

DR PROSITE; PS00018; EF_HAND; 2.

DR PROSITE; PS00019; THIOL_PROTEASE_CYS; 1.

DR PROSITE; PS00019; THIOL_PROTEASE_ASN; FALSE_NEG.

DR PROSITE; PS00639; THIOL_PROTEASE_ASN; FALSE_NEG.

DR PROSITE; PS00640; THIOL_PROTEASE_ASN; REGE.

MW Hydrolase; Thiol protease; Calcium-binding; Repeat; Multigene family;
EMBL; AF261089; AAF99682.1; -.
EMBL; BC021303; AAF31303.1; -.
EMBL; J04700; AAA52760.1; -.
PIR; S10590; CIHUH2.
PDB; 1KFU; 07-DEC-01.
PDB; 1KFX; 07-DEC-01.
MEROPS; C02.002; -.
Genew; HGNC:1479; CAPN2.
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  DOMAIN
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TISSUE-Lymph node;
MEDLINE-89197947; PubMed=2539381;
Hata A., Ohno S., Akita Y., Suzuki K.;
"Tandemly reiterated negative enhancer-like elements regulate transcription of a human gene for the large subunit of calcium dependent protease.";
J. Biol. Chem. 264:6404-6411(1989).
                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                 EMBL; M23254; AAA35645.1; -.
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wa K., Irie A., Sorimachi H., Bourenkow
   re; Polymorphism.
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27 355
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515 529
530 700
541 552
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LINKER.
DOMAIN IV.
EF-HAND 1.
                                                       THE SMALL SUBUNIT LARGE [CATALYTIC]
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kow G., Bartunik H.,
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EF-HAND 3.

ANCESTRAL CALCIUM SITE 4 (
ANCESTRAL CALCIUM SITE 5 (
BY SIMILARITY.

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IE -> MR (IN REF. 1).

Q -> K (IN REF. 2).

N -> S (IN REF. 2).

V -> F (IN REF. 3).
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5 (POTENTIAL)
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Best Local S
Matches 250
                                                                                                            Zhang J.L., Patel J.M., Block E.R.;
"Hypoxia-specific upregulation of calpain activity and gene expression in pulmonary artery endothelial cells.";
Am. J. Physiol. 275:L461-L468(1998).
-!- FUNCTION: Calcium-regulated non-lysosomal thiol-protease which catalyze limited proteolysis of substrates involved in cytoskeletal remodelling and signal tranduction (By similarity).
-!- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-l-Xaa, Met-l-Xaa, M-g-l-Xaa with Leu or Val as the P2 residue.
-!- COFACTOR: Binds 3 calcium ions.
-!- ENYIME REGULATION: Activated by 200-1000 micromolar concentratic of calcium and inhibited by calpastatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P43367;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Calpain 2, large [catalytic] subunit (EC 3.4.22.17) (Calcium-activated neutral proteinase) (CANP) (M-type) (M-calpain) (Millimolar-calpain)
                                                                                                                                                                                                                                                                                                                                              "Cloning the partial cDNAs skeletal muscle.";
Biochimie 75:931-936(1993).
                          membrane upon Ca++ binding.
-!- SIMILARITY: Contains 5 EF-hand calcium-binding
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C2.
                                                                                                                                                                                                                                                                                    TISSUE=Pulmonary artery;
MEDLINE=98400921; PubMed=9728040;
                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=94146155; PubMed=8312396;
Sun W., Ji S.Q., Ebert P.J., Bidwell C.
                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Skeletal
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Fragment).
                                                                     (regulatory) subunit.
SUBCELLULAR LOCATION: Cytoplasmic;
                                                                                                  SUBUNIT: Heterodimer of a large
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                                                                                                                                                                                                                                                                                                                                                                                                                    muscle;
  entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
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 is
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As of mu-calpain a
copyright.
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Pred. No. 2
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                                                                                                  (catalytic)
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RESULT 3
CAN2_RABIT
ID CAN2_R
AC PO6814
DT 01-JAN
DT 01-JAN
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DE Calpai
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Best Local
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InterPro; IPR001300; Protease_C2.
InterPro; IPR001300; SHprot_acsite.
Pfam; PF001067; Calpain_III; 1.
Pfam; PF001067; Calpain_III; 1.
Pfam; PF00036; efhand; 2.
PRINTS; PR00704; CALPAIN.
SMART; SM00720; calpain_III; 1.
SMART; SM00720; calpain_III; 1.
SMART; SM00730; calpain_III; 1.
PROSITE; PS00018; EF_HAND; 1.
PROSITE; PS00019; THIOL_PROTEASE_CYS; PAPROSITE; PS000639; THIOL_PROTEASE_HIS; PAPROSITE; PS000640; THIOL_PROTEASE_HIS; PAPROSITE; PS00640; THIOL_PROTEASE_HIS; PAPROSITE; PAPROSITE; PAPROSITE; PAPROSITE; PS00640; THIOL_PROTEASE_HIS; PAPROSITE; PS00640; THIOL_PROTEASE_HIS; PAPROSITE; PAPROSITE; PAPROSITE; PS00640; THIOL_PROTEASE_HIS; PAPROSITE; PAPROSITE; PAPROSITE; PAPROSITE; PAPROSITE; PS00640; THIOL_PROTEASE_HIS; PAPROSITE; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U01181;
EMBL; U71320;
HSSP; Q07009;
                   CAN2_RABIT STANDARD; PRT; 422.AA.

PG6814;

01-JAN-1988 (Rel. 06, Created)

01-JAN-1988 (Rel. 06, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)

Calpain 2, large [catalytic] submit (EC 3.4.22.17) (Calcium-activated neutral proteinase) (CANP) (M-type) (M-calpain) (Millimolar-calpain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CA_BIND
CA_BIND
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CONFLICT
SEQUENCE
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MEROPS; C02.0
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4 DLISWLCFSVL 324
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AAB17381.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1235;
Pred. No. 4.
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EF-HAND 2.
EF-HAND 3.
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DOMAIN IV.
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ANCESTRAL CALCIUM SITE 5
R -> K (IN REF. 2).
3929553239E123CF CRC64;
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PARTIAL.
PARTIAL.
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1.6e-81;
les 6;
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DOMAIN
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InterPro; IPR001300; Protease_C2.
InterPro; IPR000169; SHprot_acsite.
Pfam; PF01067; Calpain_III; 1.
Pfam; PF00036; efhand; 3.
Pfam; PF00648; Peptidase_C2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     subunits of two
J. Biol. Chem. 2
                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00704; CALPAIN.
SMART; SM00720; calpain_III; 1.
SMART; SM00054; EFh; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M13797; AAA31455.1; PIR; B24815; B24815.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Isolation and sequence analyses of cDNA clones for t subunits of two isozymes of rabbit calcium-dependent J. Biol. Chem. 261:9465-9471(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Suzuki K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Emori Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=86250902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                DOMAIN
                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                       Hydrolase
                                                                                                                                                                                                                                                                                      PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CANP) can bind Ca2+ ions.";
J. Biochem. 101:889-895(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-87279982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               catalyze limited proteolysis of substrates involved in cytoskeletal remodelling and signal tranduction (By similarity) CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Met-|-Xaa Arg-|-Xaa with Leu or Val as the P2 residue.

COFACTOR: Binds 3 calcium ions.

ENZYME REGULATION: Activated by 200-1000 micromolar concentrations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (regulatory) subunit.
SUBCELLULAR LOCATION: Cytoplasmic; Translocates
membrane upon Ca++ binding.
SIMILARITY: Contains 5 EF-hand calcium-binding
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: Heterodimer of a large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of calcium and inhibited by calpastatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Calcium-regulated non-lysosomal thiol-protease which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INE=87279982; PubMed=3038855;
mi Y., Emori Y., Kawasaki H., Suzuki K.;
hand structure-domain of calcium-activated neutral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration -
een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C02.002
                                                                                                                                                                                                                                                                                                                PS00639;
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237
252
263
263
307
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337
372
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                 AA,
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                                                                                                                                                                                                                                                                       protease;
                                                                                                                                                                                                                                                                THIOL_PROTEASE_CYS; PARTIAL.
THIOL_PROTEASE_HIS; PARTIAL.
THIOL_PROTEASE_ASN; PARTIAL.
protease; Calcium-binding; Mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=2424911;
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236
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422
274
318
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                              LINKER.

DOMAIN IV.

EF-HAND 1.

EF-HAND 2.

EF-HAND 3.

ANCESTRAL CALCIUM SANCESTRAL CAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   is not removed.
                                                                                                                                                                                                     CALPAIN.
DOMAIN III.
                 AE4FA3C48A333C41 CRC64
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                                                                                                                                                                                                                                                                  Multigene
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RESULT 4
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Best Local Similarity
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CANZ_MOUSE STANDARD,

CANZ_MOUSE STANDARD,

CANZ_MOUSE STANDARD,

COURT STANDARD,

COURT STANDARD,

CALPAIN Z, last sequence update)

15-SEP-2003 (Rel. 42, Last annotation update)

15-SEP-2003 (Rel. 42, Last annotation update)

Calpain Z, large [catalytic] subunit precursor (EC 3.4.22.17)

(Calcium-activated neutral proteinase) (CANP) (M-type) (M-cal;

(Calcium-arr-calpain) (80 kDa M-calpain subunit) (CALP80).
                                                                                       TISSUE=CNS;
Glass J.D., Nash N.R., Dry I., Culver D., Wesselingh'S.;
Glass J.D., Nash N.R., Dry I., Culver D., Wesselingh'S.;
"Cloning of m-calpain from mouse nervous system.";
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databbases.
-!- FUNCTION: Calcium-regulated non-lysosomal thiol-protease which catalyze limited proteolysis of substrates involved in cytoskeletal remodelling and signal tranduction (By similarity).
-!- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-xaa, Met-|-xaa Arg-|-xaa with Leu or Val as the P2 residue.
-!- COPACTOR: Binds 3 calcium ions.
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-BALB/C;
MEDLINE-97480729; PubMed-9339374;
Dear T.N., Matena K., Vingron M., Boehm T.;
"A new subfamily of vertebrate calpains lacking domain: implications for calpain regulation and
                                                                                                                                                                                                                                                            Submitted
                                                                                                                                                                                                                                                                                       STRAIN=BALB/c;
                                                                                                                                                                                                                                                                                                                               domain: implications for cogenomics 45:175-184(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota;
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
        (regulatory) subunit.
SUBCELLULAR LOCATION: Cytoplasmic;
membrane upon Ca++ binding.
                                                 ENZYME REGULATION: Activated by 200-1000 micromolar of calcium and inhibited by calpastatin.
SUBUNIT: Heterodimer of a large (catalytic) and a si
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Rodentia;
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No. 1e-80;
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HSSP;
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between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                     SEQUENCE
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European Bioinformatics Institute. There are no rest
by non-profit institutions as long as its content
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SM00230; CysPc; 1.
SM00054; EFh; 2.
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                                              ALEEAGFKMPCQLHQVIVARFADDQLIIDFDNFVRCLVRLETLFKIFKQLDPENTGT.EL
                                                                                    DGFSIETCKIMVDMLDSDGSGKLGLKEFYILWTKIQKYQKIYREIDVDRSGTMNSYEMRK-
                                                                                                                 QAVDDETEANTEETDANEEDIDDGFRRLFVQLAGEDAETSAFELQTTLRRVLAKRQDTKS
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NLASWLSFSVL
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IPR001300; Protease_C2.
IPR000169; SHprot_acsite.
                                    ALEEAGFKLPCQLHQVIVARFADDELIIDFDNFVRCLVRLETLFKIFKQLDPENTGTIQL
                                                                                                                                                                                                                                    700
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                                                                                                                                                                                                                                    AA;
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DOMAIN IV.
EF-HAND 1.
EF-HAND 2.
EF-HAND 3.
EF-HAND 3.
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Pred. No. 5.5e
9; Mismatches
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[4]
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Hosfield C.M., Moldoveanu T., Davies
"Calpain mutants with increased Ca2+
the role of the C(2)-like domain.";
J. Biol. Chem. 276:7404-7407(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21240297; pubMed=11342050;
Moldoveanu T., Hosfield C.M., Jia Z., Elce J.S., Dav
"Ca(2+)-induced structural changes in rat m-calpain
partial proteolysis.";
Biochim. Biophys. Acta 1545:245-254(2001).
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01-JUN-1994 (Rel. 29, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Calpain 2, large [catalytic] subunit precursor (EC 3.4.22.17)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20069318; PubMed=10601010;
Hosfield C.M., Elce J.S., Davies P.L., Jia Z.;
"Crystal structure of calpain reveals the structural basis for
                                                                                                     This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ca(2+)-dependent protease activity and a novel mode
activation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEBS Lett.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mutagenesis."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochim. Biophys. Acta 1216:81-93(1993).
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Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAPN2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arthur J.S., Gauthier S., Elce J.S.; "Active site residues in m-calpain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MUTAGENESIS OF LYS-230; LYS-234 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94032492; PubMed=8218419;
Deluca C.I., Davies P.L., Samis J.A., Elce of the control of the mean of the control of the 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Millimolar-calpain).
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                                                                                                                                                                                                                                                                                           FUNCTION: Calcium regulated non-lysosomal thiol-protease which catalyze limited proteolysis of substrates involved in cytoskeletal remodelling and signal tranduction.

CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Met-|-Xaa Arg-|-Xaa with Leu or Val as the P2 residue.

COPACTOR: Binds 3 calcium ions.

ENZYME REGULATION: Activated by 200-1000 micromolar concentratic of calcium and inhibited by calpastatin.
                                                 ween the Swiss Institute of Bioinf
European Bioinformatics Institute
                                                                                                                                              (regulatory) subunit.
SUBCELULIAR LOCATION: Cytoplasmic; Translocates
membrane upon Ca++ binding.
SIMILARITY: Contains 5 EF-hand calcium-binding
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C2.
                                                                                                                                                                                                                                                                              SUBUNIT: Heterodimer of a large (catalytic) and
                                                                           SWISS-PROT entry is copyright.
een the Swiss Institute of Bioi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18:6880-6889(1999)
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                                              ght. It is produced through a collaboration Bioinformatics and the EMBL outstation - titute. There are no restrictions on its
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sensitivity
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Best Local :
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Pfam; PF00036; efhand; 3.
Pfam; PF000364B; Peptidase_C2; 1.
PRINTS; PR00704; CALPAINI.
SMART; SM00720; calpain_III; 1.
SMART; SM00230; CysPC; 1.
SMART; SM00054; EFh; 2.
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MUTAGEN
SEQUENCE
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ACT_SITE
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DOMAIN
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MUTAGEN
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PROSITE; PS00139; THIOL_PROTEASE_CYS;
PROSITE; PS00639; THIOL_PROTEASE_HIS;
PROSITE; PS00640; THIOL_PROTEASE_ASN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3D-structure.
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InterPro; IPR000169; SHprot_acsite.
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690
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                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                         KNFFLTNRARERSDTFINLREVLNRFKLPPGEYILVPSTFEPNKDGDFCIRVFSEKKADY
                                                                                      DGFSIETCKIMVDMLDSDGSGKLGLKEFYILWTKIQKYQKIYREIDVDRSGTMNSYEMRK
                                                                                                                                             QAVDDEIEANLEEFDISEDDIDDGFRRLFAQLAGEDAEISAFELQTILRRVLAKRQDIKS
DLISWLSFSVL 700
                      DLISWLCFSVL 251
                                                      ALEEAGFKMPCQLHQVIVARFADDQLIIDFDNFVRCLVRLETLFKIFKQLDPENTGTIEL
                                                                                                                                    QTVDDEIEANIEEIEANEEDIGDGFRRLFAQLAGEDAEISAFELQTILRRVLAKREDIKS
                                                                                                                                                                               KNFFLTTRARERSDTFINLREVLNRFKLPPGEYVLVPSTFEPHKNGDFCIRVFSEKKADY
                                            ALEEAGFKLPCQLHQVIVARFADDELIIDFDNFVRCLVRLEILFKIFKQLDPENTGTIQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      equires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thiol protease;
                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                   93.5%;
                                                                                                                                                                                                                                                                      79919 MW;
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                                                                                                                                                                                                                                  Score 1210;
Pred. No. 6.
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EF-HAND 2.
EF-HAND 3.
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DOMAIN IV.
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E->S: DECREASE OF (
296B0DC3BEEF5B90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANCHORS TO THE SMALL SUBUNIT (POTENT CALPAIN 2, LARGE [CATALYTIC] SUBUNIT
                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                DECREASE OF 95% OF
DECREASE OF 10% OF
                                                                                                                                                                                                                                                                                                      LOSS OF ACTIVITY
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DECREASE OF 20%
                                                                                                                                                                                                                                                                                                                                                                      DECREASE
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5.4e-79;
hes 8;
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                                                                                                                                                                                                                                              Length 700;
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RESULT 6
CAN2_CHICK
  ALD COORDED TO COORDED
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Pfam; PF00038; efhand; 3.
Pfam; PF00048; Peptidase_C2; 1.
PRINTS; PR007704; CALPAIN.
SMART; SM00720; Calpain_III; 1.
SMART; SM00230; CysPc; 1.
SMART; SM00034; EFh; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 01-NOV-1997 (Rel. 28-FEB-2003 (Rel. Calpain 2, large (
                                                                                                                                                  PROSITE; PS00018;
PROSITE; PS00139;
PROSITE; PS00639;
PROSITE; PS00640;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAN2_CHICK Q92178;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Calliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Identification of a third ubiquitous calpain species -- chicken muscle expresses four distinct calpains.";
Biochim. Biophys. Acta 1261:381-393(1995)
-i- FUNCTION: Calcium-regulated non-lysosomal thiol-protease which
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Calpain 2, large [catalytic] subunit precursor (EC 3.4.22.17)
(Calcium-activated neutral proteinase) (CANP) (M-type) (M-calpain)
(Millimolar-calpain)
                                                                          PROPEP
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002048; EF-hand.
InterPro; IPR001300; Protease_C2.
InterPro; IPR000169; SHprot_acsite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D38026; PIR; S57194; $
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-95260862;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (regulatory) subunit.
SUBCELLULAR LOCATION: Cytoplasmic; Translocates
membrane upon Ca++ binding.
SIMILARITY: Contains 5 EF-hand calcium-binding
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  catalyze limited proteolysis of substrates involved in cytoskeletal remodelling and signal tranduction (By similarity). CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Met-|-Xaa Arg-|-Xaa with Leu or Val as the P2 residue.

COFACTOR: Binds 3 calcium ions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: Heterodimer of a large (catalytic) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENZYME REGULATION: Activated by 200\text{-}1000 micromolar concentrations of calcium and inhibited by calpastatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q07009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C02.002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
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                                                                                                                             protease;
                                                                  THIOL_PROTEASE_HIS; FALSE_NEG.
THIOL_PROTEASE_ASN; FALSE_NEG.
THOCHASE, CAlcium-binding; Multigene family.

19 ANCHORS TO THE SMALL SUBUNIT (POTENTIAL).
760 CALPAIN 2, LARGE [CATALYTIC] SUBUNIT.
                                                                                                                                                                                                    EF_HAND; 2.
THIOL_PROTEASE_CYS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=7742367;
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                       CALPAIN.
DOMAIN III.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is in no way for commercial
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                                                                                                                                                                                                                                                                                                                        RESULT 7
CANX_CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CA_BIND
CA_BIND
CA_BIND
DOMAIN
DOMAIN
ACT_SITE
ACT_SITE
ACT_SITE
                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE-85061606; PubMed=6095110;

Ohno S., Emori Y., Imajoh S., Kawasaki H., Kisaragi M.,

"Evolutionary origin of a calcium-dependent protease by
genes for a thiol protease and a calcium-binding proteir
                                      CALCIUM-BINDING DATA.
MEDLINE-87279982; PubMed=3038855;
Minami Y., Emori Y., Kawasaki H.,
                                                                       organization of the carcram acres Lett. 194:249-252(1986).
                                                                                   MEDLINE-86082358; PubMed=3000828; Emori Y., Ohno S., Tobita M., Suzuki K.; Gene structure of calcium-dependent protease retains organization of the calcium-binding protein gene.";
                                                                                                                                    Nature
[2]
                                                                                                                                                                                                                                              activated neutral proteingallus gallus (Chicken).
                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Calpain, large [catalytic] subunit (EC 3.4.22.17)
                                                                                                                                                                                                                             Archosauria;
                                                                                                                                                                                                                                       Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                               CANX_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                            NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                       P00789;
                         (CANP)
                        510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          450
                                                                                                                                                                                                                                                                                                                                                                                                                181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for a thiol protease and 312:566-570(1984).
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541
585
615
615
680
105
286
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                                                                                                                                                                                                                            Aves; Neognathae;
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                                                                                                                                                                                                                                                                                                                STANDARD;
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552
596
626
661
661
105
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286
79228
                                                                                                                                                                                                                                                       proteinase) (CANP) (Mu/M-type)
                                                                                                                                                                                                                                        Chordata;
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78
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                                                                                                                                                                                                                                                                                                                                                                             251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW.
                                 of calcium-activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN IV.
EF-HAND 1.
EF-HAND 3.
EF-HAND 3.
ANCESTRAL CALCIUM SANCESTRAL CALCIUM SANCESTRAL CALCIUM SYSIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C3AEDB39CCB56D3B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Suzuki
                                                                                                                                                                                                                                                                                                               705
                                           ×.;
                                                                                                                                                                                                                                                                                                                8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRC64;
                                 neutral
                                                                                                                                                   protein?";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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                                                                                                                                                                                                                                                                  (Calcium-
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                                                                                                                                                              Suzuki
fusion
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                                 protease
                                                                                               ancestral
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Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002048; EF-hand.
InterPro; IPR001300; Protease
InterPro; IPR00169; SHprot_a
Pfam; PF01067; Calpain_III; 1
Pfam; PF00036; efhand; 2.
                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00704;
SMART; SM00720; C
SMART; SM00230; C
SMART; SM00054; E
                                                                                                                                                      CA_BIND
CA_BIND
CA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
ACT_SITE
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This
                                                                                                                                                                                                                                                                                                                             PROSITE; PS00018; PROSITE; PS00139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X01415; CAA25658.1; PIR; A00979; CICHH. HSSP; Q07009; 1DF0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sorimachi H.,
Suzuki K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95260862; PubMed=7742367; Sorimachi H., Tsukahara T., Okada
                                                   SEQUENCE
                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                              Hydrolase;
                                                                                                                                                                                                                                                                                           PROSITE; PS00640;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEROPS; C02.003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Identification
                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Cytoplasmic; Translocates membrane upon Ca++ binding (By similarity).

TISSUE SPECIFICITY: Ubiquitously expressed.

PTM: THE N-TERMINUS IS BLOCKED.

SIMILARITY: Contains 5 EF-hand calcium-binding SIMILARITY: BELONGS TO PEPTIDASE FAMILY C2.

CAUTION: THIS PROTEIN WAS PREVIOUSLY THOUGHT TO HAS SINCE BEEN FOUND TO BE AN INTERMEDIATE FORN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Eleuropean Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: Heterodimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ă
                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00648; Peptidase_C2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPES
                                                289
705
                                                                                                                                                                                                                                                                                                                                           18;
                                                   AA;
                                                                                                                                                                                                                                                                                                                                                               CysPc;
EFh; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of a third ubiquitous calpain species --
s four distinct calpains.";
                                            358
5317
533
704
556
600
630
665
695
108
265
289
289
                                                                                                                                                                                                                                                                                                                                                                               calpain_III;
CysPc; 1.
                                                                                                                                                                                                                                                                          protease;
                                                                                                                                                                                                                                                                                                                                                                                                                    CALPAIN
                                                                                                                                                                                                                                                                                       EF_HAND; 1.
THIOL_PROTEASE_CYS; 1.
THIOL_PROTEASE_HIS; FALSE_NEG.
THIOL_PROTEASE_ASN; FALSE_NEG.
 61.8%;
58.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHprot_acsite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EF-hand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protease_C2.
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of large (catalytic) and
                                                   MW;
                                                                                                                                                                                                                                                                          Calcium-binding; Multigene
                                                                LINKER.

DOMAIN IV.

EF-HAND 1.

EF-HAND 2.

EF-HAND 3.

EF-HAND 3.

ANCESTRAL CALCIUM SANCESTRAL CALCIUM SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Okada-Ban M.,
                Score 799.5;
                                                                                                                                                                                                                                        DOMAIN III.
                                                                                                                                                                                                                                                          CALPAIN
                                                   ABCDDC56298E48AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Translocates
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                 DΒ
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                SITE
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                                                   CRC64;
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                Length
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                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                          family.
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                                                                                                                      (POTENTIAL)
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                   705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is
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Matches

al Similarity 146; Conserv

Conservative

58;

Mismatches

46;

Indels

1;

Gaps

Pred.

NO.

le-49;

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CANIMAN 8
CANIMAN 8
CANIMAN 8
CANIMAN 9
CANIMAN 16-0
DT 16-0
DT 16-0
DT 28-F
DE CAPN
OS MUS
OC EUKA
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RA POILT
RA DUCA
RA SANT
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CC -!-
CC -
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03550; 088666;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Calpain 1, large (catalytic) submit (EC 3.4.22.17) (Calcium-activated Calpain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LMOUSE
                                                                                                                                                                                                                                                          between
the Euro
                         EMBL; AF021847; AAB72222.1;
EMBL; AF084459; AAC33134.1;
HSSP; Q07009; 1DF0.
                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                   This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mu-calpain large subunit protein.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sanr K.E., Andrabi S., Peters L.L., Chishti A.H.; "Cloning and characterization of the cDNA and genucalpain large subunit protein."; "Submitted Andreas and the control of the cDNA and genucalpain large subunit protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neutral proteinase) (CAN CAPN1 OR CANP1 OR CANP1 OR CAPA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Poirier C., Poussard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CF-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Calcium-regulated non-lysosomal thiol-protease catalyze limited proteolysis of substrates involved in cytoskeletal remodelling and signal thiouction. CATALYTIC ACTIVITY: Preferential cleavage: Tyr-(-Xaa, Met Arg-|-Xaa with Leu or Val as the P2 residue. COFACTOR: Binds 3 calcium ions (By similarity).
                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                 membrane upon Ca++ binding (By similarity).
SIMILARITY: Contains 5 EF-hand calcium-binding domains
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (regulatory) subunit.
SUBCELLULAR LOCATION: Cytoplasmic; Translocates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENZYME REGULATION: Activated by micromolar concentrations calcium and inhibited by calpastatin. SUBUNIT: Heterodimer of a large (catalytic) and a small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    musculus (Mouse)
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D., Pinset C., Guenet J.-L.;
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Best Local (
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P97571;
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DOMAIN
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PROSITE;
                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Calpain 1, large [catalytic] subunit (EC 3.4.22.17) (Calcium-activated neutral proteinase) (CANP) (Mu-type) (muCANP) (Micromolar-calpain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00704; CALPAIN.
SMART; SM00720; calpain_III; 1.
SMART; SM00230; CysPc; 1.
SMART; SM00054; EFh; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001300; Protease_C2.
InterPro; IPR000169; SHprot_acsite.
Pfam; PF01067; Calpain_III; 1.
Pfam; PF00036; efhand; 3.
Pfam; PF00648; Peptidase_C2; 1.
                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                        CAPNI OR CLS1.
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                                  NCBI_TaxID=10116;
                                                                                     Rattus norvegicus (Rat)
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PS00018; THIOL_PROTEASE_CYS;
PS00639; THIOL_PROTEASE_HIS;
PS00640; THIOL_PROTEASE_ASN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KNFFLTNRARERSDTFINLREVLNRFKLPPGEYILVPSTFEPNKDGDFCIRVFSEKKADY
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EF-HAND 2.
EF-HAND 3.
EF-HAND 3.
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DOMAIN IV.
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Pred. No. 7.
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                                                   Craniata; Vertebrata;
Sciurognathi; Muridae
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                                                                                                                                                                                                                                                                                         ACT_SITE
ACT_SITE
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SMART; SM00230; CysPc; 1.
SMART; SM00054; EFh; 3.
PROSITE; PS00018; EF_HAND; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00036; efhand; 3.
Pfam; PF00648; Peptidase_C2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001300; Protease_C2.
InterPro; IPR000169; SHprot_acsite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (regulatory) subunit.
SUBCELLULAR LOCATION: Cytoplasmic; Translocates membrane upon Ca++ binding (By similarity).
SIMILARITY: Contains 5 EF-hand calcium-binding SIMILARITY: BELONGS TO PEPTIDASE FAMILY C2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Calcium-regulated non-lysosomal thiol-protease which catalyze limited proteolysis of substrates involved in cytoskeletal remodelling and signal tranduction.

CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Met-|-Xaa Arg-|-Xaa with Leu or Val as the P2 residue.

COFACTOR: Binds 3 calcium ions (By similarity).

ENZYME REGULATION: Activated by micromolar concentrations of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        calcium and inhibited by calpastatin SUBUNIT: Heterodimer of a large (cata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1KXR; 20-MAI
PS; C02.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EM
                                      521
                                                                                                                     461
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                                                                                                                                                                                                140;
                                                                               61
                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PR00704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and this statement is not removed requires a license agreement (See an email to license@isb-sib.ch).
                                                                                                                 KNFFLTNRARERSDTFINLREVLNRFKLPPGEYILVPSTFEPNKDGDFCIRVFSEKKADY
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                                      QELDDQIQANLPDEKVLSEEEIDDNFKTLFSKLAGDDMEISVKELQTILNRIISKHKDLR
                                                          QAVDDEIEANL-EEFDISEDDIDDGFRRLFAQLAGEDAEISAFELQTILRRVLAKRQDIK
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SDGFSIETCKIMVDMLDSDGSGKLGLKEFYILWTKIQKYQKIYREIDVDRSGTMNSYEMR
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THIOL_PROTEASE_HIS; FALSE_NEG.
THIOL_PROTEASE_ASN; FALSE_NEG.
Hydrolase; Thiol protease; 3D-s
                                                                                                                                                                                                                59.7%;
56.7%;
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                                                                                                                                                                                                                                                                                                                                                EF-HAND 1.
EF-HAND 2.
EF-HAND 3.
ANCESTRAL CALCIUM SANCESTRAL CALCIUM 
                                                                                                                                                                                                                                                                                                                                                                                                                                               LINKER.
DOMAIN IV.
                                                                                                                                                                                                                Pred.
                                                                                                                                                                                                                                Score 772.5;
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BY
BY
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SIMILARITY.
SIMILARITY.
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(See http://www.isb-sib.ch/announce/
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4 (POTENTIAL).
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InterPro;
InterPro;
InterPro;
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01-JAN-1988 (Rel. 06, Last sequence update)
08-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Calpain 1, large [catalytic] subunit (EC 3.4.22.17) (Calcium-activated)
                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restitute the curopean Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                  J. Biochem. 101:889-895(1987).

- FUNCTION: Calcium regulated non-lysosomal thiol-protease catalyze limited proteolysis of substrates involved in cytoskeletal remodelling and signal tranduction.

- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Met Arg-|-Xaa with Leu or Val as the P2 residue.

-- COFACTOR: Binds 3 calcium ions (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDJUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-86250902; PubMed-2424911;
KAWASAKI H., Sugihara H
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                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
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J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neutral proteinase) (CANP) (Mu-type) (muCANP) (Micromolar-calpain)
                                                                                       EMBL; M13363; AAA31456.1; PIR; A24815; A24815.
                                                                                                                                                               modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minami Y., Emori Y., Kawasaki H., Suzuki K.; 
"E-F hand structure-domain of calcium-activated (CANP) can bind Ca2+ ions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-87279982; Put
Minami Y., Emori Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                          MEROPS; C02.001;
                                                                                                   EMBL; M13363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CALCIUM-BINDING DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Isolation and sequence analyses of cDNA clones for the large subunits of two isozymes of rabbit calcium-dependent protease."; Biol. Chem. 261:9465-9471(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10
                                                                                                                                                                                                                                                membrane upon Ca++ binding (By similarity) SIMILARITY: Contains 5 EF-hand calcium-bin SIMILARITY: BELONGS TO PEPTIDASE FAMILY C2
                                                                                                                                                                                                                                                                                                                      ENZYME REGULATION: Activated by micromolar concentrations calcium and inhibited by calpastatin.
SUBUNIT: Heterodimer of a large (catalytic) and a small
                                                                                                                                                                                                                                                                                            (regulatory) subunit.
SUBCELLULAR LOCATION: Cytoplasmic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240
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; IPR001300;
; IPR000169;
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Chordata; Craniata; Ve
Lagomorpha; Leporidae;
                                             EF-hand
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                                                                                                                                               (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                             Translocates
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me; Oryctolagus
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01300; Protease_C2. 00169; SHprot_acsite. Calpain_III; 1.

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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                              FEBS
                                                                    MEDILINE=86301172; PubMed=3017764;
Aoki K., Imajoh S., Ohno S., Emori Y., Koike M., Kosaki G., Suzuki |
"Complete amino acid sequence of the large subunit of the low-Ca2+-
requiring form of human Ca2+-activated neutral protease (muCANP)
deduced from its cDNA sequence.";
TEBS Lett. 205:313-317(1986).
                                                                                                                        SEQUENCE FROM N.A. MEDLINE=86301172;
                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                     Homo sapiens (Human).
                                                                                                                                                                                               neutral proteinase) (CANP) (Mu-type) (muCANP) (Micromolar-calpain). CAPN1 OR CANPL1.
                                                                                                                                                                                                                 01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Calpain 1, large [catalytic] subunit (EC 3.4.22.17) (Calcium-activated
                                                                                                                                                                                                                                                          P07384;
                                                                                                                                                                                                                                                                      CAN1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase;
 Minami Y., Suzuki K.;
"A novel member of the calcium-dependent cysteine
Biol. Chem. Hoppe-Seyler 371:171-176(1990).
                    Minami Y.,
                                                    SEQUENCE FROM
                                                                                                                                                       NCBI_TaxID=9606;
                               Sorimachi H., Ohmi
                                         MEDLINE=90380278; PubMed=2400579;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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; SM00720; calpain_III;
; SM00054; EFh; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138;
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PS00139;
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                                                                                                                                                                                                                                                                                                                                                                      KALEEAGFKMPCQLHQVIVARFADDQLIIDFDNFVRCLVRLETLFKIFKQLDFENTGTIE
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THIOL_PROTEASE_HIS;
THIOL_PROTEASE_ASN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EF_HAND;
                             s.,
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130
301
153
197
227
262
292
                                                                                                                                                                Chordata;
Primates;
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55.9%;
                               Emori Y.,
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DOMAIN IV.

EF-HAND 1.

EF-HAND 2.

EF-HAND 3.

ANCESTRAL CALCIUM SITE 4 (POTENTIAL).

ANCESTRAL CALCIUM SITE 5 (POTENTIAL).

MW; 178BFEF4216C6EAB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Calcium-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 2.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 759.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN III.
                                                                                                                                                                Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                    PRT;
                               Kawasaki H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PARTIAL.
PARTIAL.
PARTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .7e-47;
                                                                                                                                                                Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Multigene
                              Saido T.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 302;
          protease family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                          Euteleostomi;
                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  family.
                                Ohno
                                                                                                               Suzuki K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                      179
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RA Strausberg R.L., Felipold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Raw S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Raw S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan R., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,
RA Willalon D.K., McEwan P.J., Malek J.A., Gunaratne P.H.,
RA Willalon D.K., McEwan P.J., Malek J.A., Gubs R.A.,
RA Willalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Willalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Willalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Willalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Willalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Willalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Willalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Willalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Willalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Willalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Willalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Willalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Willalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Willalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Willalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Ra Willalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Ra Willalon D.K., Mozly D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Ra Willalon D.K.,
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SEQUENCE /
                                                                             PROSITE;
PROSITE;
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PROSITE;
                                                                                                                                                                                                                                                                                                            InterPro;
InterPro;
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MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Gr
                                                                                                                                                                                                                      Pfam; PF01067; Calpain II; 1
Pfam; PF00036; efhand; 3.
Pfam; PF00648; Peptidase_C2;
PRINTS; PR00704; CALPAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
DOMAIN
DOMAIN
                                                                                                                                                            SMART; SM00720; calpain_III; 1.
SMART; SM00230; CysPc; 1.
SMART; SM00054; EFh; 3.
                                                                                                                                                                                                                                                                                                                                                                                              MIM;
                                                                                                                                                                                                                                                                                                                                                     GO; GO:0008284; P:positive regulation InterPro; IPR002048; EF-hand.
                                                                                                                                                                                                                                                                                                                                                                                                                 Genew; HGNC:1476;
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A26213; CIHUH.
HSSP; Q07009; 1DF0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X04366; CAA27881.1; -
EMBL; BC008751; AAH08751.1;
                                                              Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              membrane upon Ca++ binding (By similarity). SIMILARITY: Contains 5 EF-hand calcium-binding SIMILARITY: BELONGS TO PEPTIDASE FAMILY C2.
                                                                                                                                                                                                                                                                                                                                                                                                                                         C02.001;
                                                                                 PS00640;
                                                                                                    PS00639;
                                                                                                                          PS00139;
                                                                                                                                                                                                                                                                                                          IPR001300; Protease_C2.
IPR000169; SHprot_acsite.
                                                         Thiol protease;
30
366
527
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1DF0.
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                                                                             THIOL_PROTEASE_CYS; 1.
THIOL_PROTEASE_HIS; FALSE_NEG.
THIOL_PROTEASE_ASN; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                   CAPN1
                                                                                                                                         EF_HAND;
365
526
542
                                                         Calcium-binding; Multigene family.
                                        CALPAIN.
                     DOMAIN III.
                                                                                                                                                                                                                                                                                                                                                                        of cell proliferation; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Abramson R.D., Mullahy S.J.,
Malek J.A., Gunaratne P.H.,
a A.M., Gay L.J., Hulyk S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T.E.,
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RESULT 12
CAN1_PIG
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Best Local S
Matches 137
                                                                                                                                                         SEQUENCE FROM N.A.
Smith T.P.L., Simmen F.A., Vallet J.A.;
Smith T.P.L., Simmen F.A., Vallet J.A.;
"Rapid Communication: nucleotide sequences of micromolar calcium-activated neutral protease micromolar calcium-activated neutral protease processes with the EMBL/GenBank/DDBJ to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
CA_BIND
CA_BIND
CA_BIND
DOMAIN
DOMAIN
ACT_SITE
ACT_SITE
ACT_SITE
CONFLICT
                                                                                                                                                                                                                                                                                                  P35750; Q29600; Q9NOM6;
01-JUN-1994 (Rel. 29, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Calpain 1, large [catalytic] subunit (EC 3.4.22.17) (Calcium-activated)
                                                                                                                                                                                                                                                                                                                                               CAN1_PIG
P35750; C
                      MEDLINE-94146155; PubMed-8312396; Sun W., Ji S.Q., Ebert P.J., Bidwell C.A. "Cloning the partial cDNAs of mu-calpain skeletal muscle.", Biochimie 75:931-936(1993).
                                                                                                                             TISSUE=Small intestine; Winteroe A.K., Fredholm
                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                     Sus scrota (Pig).
                                                                                                                                                                                                                                                                                  CAPN1
                                                                                                                                                                                                                                                                                         neutral proteinase) (CANP) (Mu-type) (muCANP) (Micromolar-calpain).
                                                                                                                     Submitted
                                                                                     TISSUE=Skeletal
           FUNCTION: Calcium-regulated r catalyze limited proteolysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                        642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      462
                                                                                                                                                                                                                                                                                                                                                                                                               702
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137; Conserv
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VELDDQIQANLFDEQVLSEEEIDENFKALFRQLAGEDMEISVKELRTILNRIISKHKDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KALEEAGFKMPCQLHQVIVARFADDQLIIDFDNFVRCLVRLETLFKIFKQLDPENTGTIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDGFSIETCKIMVDMLDSDGSGKLGLKEFYILWTKIQKYQKIYREIDVDRSGTMNSYEMR
                                                                                                                                                                                                                                                                                                                                                                                                                                    LDLISWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TKGFSLESCRSMVNLMDRDGNGKLGLVEFNILWNRIRNYLSIFRKFDLDKSGSMSAYEMR
                                                                                                                                                                                                                                                                                                                                                                                                               FDLFKWL
                                                                                                                    (AUG-1995)
                                                                                                528-623
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                                                                                                                   Fredholm
-1995) to
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                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                     muscle;
 remodelling
                                                                                                                                                   FROM
                                                                                                                                                                                                                                               Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81889
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55.5%;
                                                                                                                   the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57;
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EF-HAND 2.

EF-HAND 3.

ANCESTRAL CALCIUM S
ANCESTRAL CALCIUM S
ANCESTRAL IT.

By similarity.

By similarity.

By similarity.

By similarity.

By similarity.
                                                                                                                   Davies W.;
EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -> N (IN REF. 3).
1CB6D7C56D063498
non-lysosomal thiol-protease s of substrates involved in d signal tranduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          757.5;
No. 9.
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                                                    1., Hancock
1 and m-calp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .9e-47;
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                                                                                                                                                                       f two isoforms c
l (mucalpain)
databases.
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                                                                                                                    databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC64;
                                                  k D.
lpa:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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                                                                                                                                                                                                                                                 Euteleostomi; Sus.
                                                    ín.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                     from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   714;
                                                                                                                                                                                  of porcine
) cDNA.";
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                                                     porcine
                       which
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Best Local S
Matches 137
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InterPro; IPR002048; EF-hand.
InterPro; IPR001300; Protease_(
InterPro; IPR00150; SHprot_ac;
Pfam; PF00167; Calpain_III; 1.
Pfam; PF00036; efhand; 3.
Pfam; PF000648; Peptidase_C2; 1
PRINTS; PR00704; CALPAIN.
SMART; SM00720; Calpain_III; 1
SMART; SM00730; CysPc; 1.
SMART; SM00730; EFF; 3.
SMART; SM00054; EFF; 3.
                                                                                                                                                                                                                                                                                       CA_BIND
CA_BIND
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CONFLICT
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DOMAIN
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (regulatory) subunit.
SUBCELLULAR LOCATION: Cytoplasmic; Translocates
membrane upon Ca++ binding (By similarity).
SIMILARITY: Contains 5 EF-hand calcium-binding
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arg-|-Xaa
COFACTOR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENZYME REGULATION: Activated by micromolar calcium and inhibited by calpastatin. SUBUNIT: Heterodimer of a large (catalytic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U01180;
Q07009;
                                           120
                                                                                522
                                                                                                                                                                                                                       137;
                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF263610; AAF73444.1; -. F14611; CAA23154.1; -.
                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS00018; EF_HAND; 2.
PS00139; THIOL_PROTEASE_CYS;
PS00639; THIOL_PROTEASE_HIS;
PS00640; THIOL_PROTEASE_ASN;
TKGFSLESCRSMYNLMDRDGNGKLGLVEFNILWNRIRNYLSIFRKFDLDKSGSMSAYEMR
                                                                                                                                                  SDGFSIETCKIMVDMLDSDGSGKLGLKEFYILWTKIQKYQKIYREIDVDRSGTMNSYEMR
                                                                                QELDDQVQAILPDEQVLSEEEIDENFKALFRQLAGEDMEISVRELRTILNRIISKHKDLR
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366
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Binds 3 calcium ions (By :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1DF0
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AAA65125.1;
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526
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704
7115
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81738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protease;
                                                                                               -EEFDISEDDIDDGFRRLFAQLAGEDAEISAFELQTILRRVLAKRQDIK
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55
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SHprot_acsite
                                                                                                                                                                                                                                        5.55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Preferential cleavage: Tyr-|-Xaa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ROTEASE_CYS; 1.
ROTEASE_HIS; FALSE_NEG.
ROTEASE_ASN; FALSE_NEG.
; Calcium-binding; Multi
                                                                                                                                                                                                                                                                                           WW.
                                                                                                                                                                                                                     57;
                                                                                                                                                                                                                                                                                                    ANCESTRAL CALCIUM S
ANCESTRAL CALCIUM S
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
V > I (IN REF. 3).
I -> N (IN REF. 3).
C -> G (IN REF. 3).
S -> A (IN REF. 3).
                                                                                                                                                                                                                                        Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EF-HAND 1.
EF-HAND 2.
EF-HAND 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LINKER.
DOMAIN IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                       V -> I (IN REF. 3).
I -> N (IN REF. 3).
E -> G (IN REF. 3).
S -> A (IN REF. 3).
OBB31DE4FC56363A
                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                        756.5;
No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       III.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Translocates
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                                                                                                                                                                                                                    .2e-46;
nes 52;
                                                                                                                                                                                                                                                        DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Multigene
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                                                                                                                                                                                                                                                        1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and
                                                                                                                                                                                                                                                                                           CRC64;
                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                     Indels
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                                                    PROSITE; PS00018; E
PROSITE; PS00139; 7
PROSITE; PS00639; 7
PROSITE; PS00640; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).

Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele

Eukaryota; Metazoa; Chordata; Craniata; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CANB_HUMAN
Q9UMQ6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _HUMAN
                                                                                                                                                                     InterPro; IPR002048; EF-hand.
InterPro; IPR001300; Protease_C2.
InterPro; IPR000169; SHprot_acsite.
Pfam; PF01067; Calpain_III; 1.
Pfam; PF00036; efhand; 2.
Pfam; PF00048; Peptidase_C2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Calpain 11 (EC 3.4.22.17) (Calcium-activated neutral proteinase 11)
                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institumodified and this statement entities requires a license
                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomics 59:243-247(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=99339989; Pubn
Dear T.N., Moller A.,
                        Hydrolase;
DOMAIN
                                                                                                                                                         PRINTS; PR00704;
                                                                                                                                                                                                                                                                                          Genew; HGNC:1478; CAPN11
                                                                                                                                                                                                                                                                                                         MEROPS;
                                                                                                                                                                                                                                                                                                                       EMBL; AJ242832; CAB52137.1; HSSP; Q07009; 1DF0.
                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chromosome 6."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dear T.N., Moller A., Boehm T.;
"CAPN11: A calpain with high mRNA levels in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CANP 11).
                                                                                                                                                                                                                                                            GO:0004198; F:calpain activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY: HIGHEST EXPRESSION IN TESTIS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C2.
SIMILARITY: Contains 4 EF-hand calcium-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        catalyze limited proteolysis of substrates involved in cytoskeletal remodelling and signal tranduction. CATALYTIC ACTIVITY: Preferential cleavage: Tyr-1-Xaa, Arg-1-Xaa with Leu or Val as the P2 residue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: Heterodimer of a large (catalytic) and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Calcium-regulated non-lysosomal thiol-protease which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (regulatory) subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240
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                                                                                                              SM00720; calpain_III; 1.
SM00230; CysPc; 1.
SM00054; EFh; 2.
                                                                                                                                                                                                                                                                                                         C02.013;
                                                    PS00018; EF_HAND; UNKNOWN_2.
PS00139; THIOL_PROTEASE_CYS;
PS00639; THIOL_PROTEASE_HIS;
PS00640; THIOL_PROTEASE_ASN;
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                                         Thiol
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                                      protease;
                                                                                                                                                          CALPAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=10409436;
                          352
                                                                                                                                                                                                                                                                                                                                                                               license agreement (See
                                    OTEASE_HIS; FALSE_NEG.
OTEASE_ASN; FALSE_NEG.
Calcium-binding; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T.;
                                                                                                                                                                                                                                                                                                                                                                                                is not removed
                          CALPAIN
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CAN3_CHICK
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Best Local 9
                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
28-FEB-2003 (Rel. 4.
Calpain 3 large auth
                                                                                                                                                                                                                                                                                                                                                                                   CAN3_CHICK 092177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
CA_BIND
CA_BIND
DOMAIN
DOMAIN
ACT_SITE
ACT_SITE
ACT_SITE
                                                                                                              "Identification of a third ubiquitous calpain species -- chic muscle expresses four distinct calpains.";
Biochim. Biophys. Acta 1261:381-393(1995).
-i- FUNCTION: Calcium-regulated non-lysosomal thiol-protease.
                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Calpain 3 large subunit (EC 3.4.22.17) (Calpain L3) (Calpain p94, large [catalytic] subunit) (Calcium-activated neutral proteinase 3)
(CANP 3) (Muscle-specific calcium-activated neutral protease 3 large
 + + +
                                                                                                                                                                        Sorimachi H.,
                                                                                                                                                                                    TISSUE-Lung;
MEDLINE-95260862;
                                                                                                                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                                                                        Archosauria; Aves;
                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                              Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                     subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN

    -!- CATALYTIC ACTIVITY: Preferential cleavage: 1
Arg-|-Xaa with Leu or Val as the P2 residue.

                                                                                                                                                                                                                                 NCBI_TaxID=9031;
(regulatory) subunit.
SUBCELLULAR LOCATION: Cytoplasmic an
TISSUE SPECIFICITY: SKELETAL MUSCLE.
INVESTINE AND BONE.
SIMILARITY: Contains 4 EF-hand calci
                                                     ENZYME REGULATION: Activated by micro calcium and inhibited by calpastatin SUBUNIT: Heterodimer of a large (cata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   630
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586
616
651
681
102
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283
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                                                                                                                                                                                                           N.A.
                                                                                                                                                                         Tsukahara T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΑA;
                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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701
597
627
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662
102
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                                                                                                                                                                                    PubMed=7742367;
                                                                                                                                                                                                                                                        Neognathae;
                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata;
Neognathae; Galliformes; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.0%;
                                                                              Activated by micromolar
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DOMAIN IV.

EF-HAND 1.

EF-HAND 2.

ANCESTRAL CALCIUM S
ANCESTRAL CALCIUM S
ANCESTRAL TALCIUM S
BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.
                                                                                                                                                                         Okada-Ban
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 646.5;
Pred. No. 7.6
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 calcium-binding
                                                       (catalytic) and
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                        MOT
                                    nuclear
                                                                                                                                                                          Sugita
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                                                                                                                                                                                                                                                         Phasianidae;
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                        LEVELS
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                                                                                                     Tyr-|-Xaa, Met-|-Xaa
                                                                               concentrations
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  domains
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idae; Phasianinae;
                      IN SPLEEN
                                                                                                                                                                          Ishiura
                                                          small
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                                                                                                                                                   chicken
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RESULT 15
CAN3_HUMAN STANDARD;
ID CAN3_HUMAN STANDARD;
AC P20807; Q9Y5S6; Q9Y5S7;
DT 01-FEB-1991 (Rel. 17, Created)
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Best Local S
Matches 114
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CA_BIND
DOMAIN
DOMAIN
ACT_SITE
ACT_SITE
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SMART; SM00720; calpain_III; 1.

SMART; SM00230; CysPc; 1.

SMART; SM00034; EFh; 3.

PROSITE; PS00018; EF_HAND; 2.

PROSITE; PS00139; THIOL_PROTEASE_HIS; FALSE_NEG.

PROSITE; PS00639; THIOL_PROTEASE_ASN; FALSE_NEG.

PROSITE; PS00640; THIOL_PROTEASE_ASN; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam;
Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics including as its content is enough as its content in endified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement as itcense agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between the Swiss Institute of Bioinf
the European Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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PF00036;
PF00648;
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IPR001300; Protease_C2.
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CALPAIN III.

LINKER.

LINKER.

DOMAIN IV.

EF-HAND 1 (PROBABLE).

EF-HAND 2 (PROBABLE).

ANCESTRAL CALCIUM SITE 3

ANCESTRAL CALCIUM SITE 4

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RA Richard I., Broux O., Allamand V., Fougerousse F., Chiannilkulchai N., Bourg N., Brenguier L., Devaud C., RA Tischfield J.A., Fardeau M., Jackson C.E., Cohen D., Beckmann T "Mutations in the proteolytic enzyme calpain 3 cause limb--- Cell 81:27-40(1995).
    REPRESENTATION OF THE PROPERTY OF THE PROPERTY
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  Dincer P., I
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Roudaut C.,
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Mignard D., de
Beckmann J.S.;
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island
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1996 (Rel. 33, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Calpain 3 large subunit (EC 3.4.22.17) (Calpain L3) (Calpain p94, large [catalytic] subunit) (Calcium-activated neutral proteinase (CANP 3) (Muscle-specific calcium-activated neutral protease 3 la subunit) (nCL-1).
CAPN3 OR CANP3 OR CANPL3 OR NCL1.
                                                                                                                                                                                                                        MEDLINE=97294404; PubMed=9150160;
Richard I., Brenguier L., Dincer P.,
Burgunder J.-M., Chemaly R., Garcia (
Kurnit D.M., Lefranc G., Legum C., La
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                                                                                                                       "Multiple independent molecular etiology dystrophy type 2A patients from various g Am. J. Hum. Genet. 60:1128-1138(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANTS LGMD2A GLN-572 AND GLY-744.
WEDLINE-96176567; PubMed=8624690;
Fardeau M., Hillaire D., Mignard C.,
Mignard D., de Ubeda B., Collin H.,
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distinct from both m- and
in skeletal muscle.";
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Eukaryota; Metazoa; C
                                                          VARIANTS LGMD2A ASN-336; GLN-490; MEDLINE-97410018; PubMed-9266733;
                                                                                                                                                                                    Beckmann J.
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[5]
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                    410018; PubMed=9266733;
Leturcg F., Richard I.,
Akcoeren Z., Broux O.
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   Chemaly R., Garcia C.A., Halaby G., Jacksc
ranc G., Legum C., Loiselet J., Merlini L.,
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"Clinical, pathological, and genetic features of limb-girdle m dystrophy type 2A with new calpain 3 gene mutations in seven p from three Japanese families.";
Muscle Nerve 21:1493-1501(1998).
-!- FUNCTION: Calcium-regulated non-lysosomal thiol-protease.
-!- CATALYTIC ACTIVITY: Preferential Cleavage: Tyr-|-Xaa with Leu or Val as the P2 residue.
-!- Arg-|-Xaa with Leu or Val as the P2 residue.
-!- ENZYME REGULATION: Activated by micromolar concentrations calcium and inhibited by calpastatin.
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"A small in frame deletion within the protease domain of muscle-
specific calpain, p94 causes early-onset limb-girdle muscular
dystrophy 2A.";
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MEDLINB-98433925; PubMed=9762961;
Urtasun M., Saenz A., Roudaut C., Poza J.J., Urti
Cobo A.-M., Richard I., Garcia Bragado F., Leturc
Marti Masso J.F., Beckmann J.S., Lopez de Munain
"Limb-girdle muscular dystrophy in Guipuzcoa (Bas
Spain).";
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Kawajiri M., Nishida Y., Endo I., Kashiwagi S., Nishino H.,
Fujiwara T., Okuno S., Roudaut C., Richard I., Beckmann J.S.,
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                                                                                                                                        TISSUE SPECIFICITY: Skeletal muscle.

DISEASE: Defects in CAPN3 are the cause of limb-girdle muscular dystrophy type 2A (LGMD2A) [MIM:253600]. LGMD2A is both autosomal dominantly and recessively transmitted. It is characterized by progressive symmetrical atrophy and weakness of the proximal limb muscles and elevated serum creatine kinase. The symptoms usually begin during the first two decades of life, and the disease gradually worsens, often resulting in loss of walking ability 10 or 20 years after onset.

SIMILARITY: Contains 4 EF-hand calcium-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                        (regulatory) subunit.
SUBCELLULAR LOCATION: Cytoplasmic.
ALTERNATIVE PRODUCTS:
                                                                                                           DATABASE: NAME=Leiden Muscular Dystrophy
              European
                                                                   NOTE=Calpain-3 mutations in LGMD2A; WWW-"http://www.dmd.nl/capn3_home.html"
                                                                                                                             SIMILARITY: BELONGS TO PEPTIDASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: Heterodimer of a large (catalytic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dell K.P., Kaplan J.-C., Beckmann J.S., Topaloglu H.;
dochemical, genetic, and clinical survey of autosomal recessive
girdle muscular dystrophies in Turkey.";
Neurol. 42:222-229(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=3;
          SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the ENsuropean Bioinformatics Institute. There are no restr
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SMART; SM00720; calpain_III; 1
SMART; SM00720; cyspc_1;
SMART; SM00230; Cyspc_1;
SMART; SM00054; EFh; 3.

PROSITE; PS00018; EF_HAND; 2.
PROSITE; PS00139; THIOL_PROTEA;
PROSITE; PS00639; THIOL_PROTEA;
PROSITE; PS00640; THIOL_PROTEA;
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GO:0004108; F:calpain activity; TAS.
GO:0008234; F:cysteine-type peptidase activity;
GO:0004871; F:signal transducer activity; TAS.
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; Polymorphism; Alternative splicing.
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                                              calpain (EC 3.4.22 calpain (EC 3
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tissue-specific ca calmodulin-related	D96689	22	157	8. 4.4	108.5	4 4 5 4
calcium-dependen	A43713	ч	508	. 6	109	43
calcium-dependent	T03024	ш	465	8.4	109	42
probable calmodui	T02887	N	187	8.4	109	41
calmodulin (cam2)	н84667	N	149	8.4	109	40
calmodulin [simila	S22503	L	149	8.4	109	39
calmodulin - leaf	S53006	_	149	8.4	109	38
Spec-related prote	A31797	ᆫ	317	8.5	110	37
hypothetical prote	H86194	N	150	8.5	110.5	36
slow cardiac trop	JW0066	N	162	8.6	111	35
calmodulin 2 (clo	S22860	N	149	8.6	111	34
centrin ICL1c - Pa	S71319	N	183	8.6	111.5	ω
calmodulin - Pneu	JN0722	N	151	8.6	111.5	32
probable calcium	F85059	N	520	8.8	114.5	31
protein kinase, ca	T14335	ν	532	9.0	116	30

ALIGNMENTS

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F; 105, 262, 286/		F;2-700/Product F;75-327/Domain F;529-560/Doma	A; Description: A; Note: cleaves C; Superfamily: C: Keywords: Act	A;Gene: GDB:CAPN2; mCANP; CAPN2; COB:119 A;Cross-references: GDB:119 A;Map position: lpter-lqter C;Complex: heterodimer of L C;Function:	A; Molecule type: DN A; Residues: 1-67, 'G A; Cross-references: C: Genetics:	J. Biol. Chem. A; Title: Tander A; Reference nur A: Accession: A	A; Molecule type A; Residues: 1- A; Cross-reference A; Crote: parts Crote: parts	A; Molecule type: mRNA A; Residues: 1-700 < SOR> R; Imajoh, S.; Aoki, K.; Biochemistry 27, 8122-8 A; Title: Molecular clon A; Reference number: A3128 A; Accession: A31218	RESULT 1 CIHUH2 Calpain (EC 3.4.22.17) large calpain (EC 3.4.22.17) large N;Alternate names: calpain ch C;Species: Homo sapiens (man) C;Date: 21-Nov-1993 #sequence C;Accession: \$10590; A31218; R;Sorimachi, H.; Ohmi, S.; Em Biol. Chem. Hoppe-Seyler 371(A;Title: A novel member of th A;Reference number: \$10589; M A;Accession: \$10590
105,262,286/Active site: Cys, His,	572-604/Domain: calmodulin repeat h 605-634/Domain: calmodulin repeat h 637-669/Domain: calmodulin repeat h 637-669/Domain: calmodulin repeat h	2-700/Product: calpain large chain 2 #status predicted 75-327/Domain: calpain catalytic domain homology <calp> 529-560/Domain: calmodulin repeat homology <efi></efi></calp>	A;Description: catalyzes the hydolysis of peptides A;Note: cleaves preferentially after tyrosine, met C;Superfamily: calpain large chain; calmodulin rep C;Superfamily: calpain large end: calcium hinding:	A;Gene: GDB:CAPN2; mCANP; CANPml A;Cross-references: GDB:119750; OMIM:114230 A;Amp position: lpter-lqter C;Complex: heterodimer of L (large) and S (C;Complex: heterodimer of L)	E: DNA 57,'G',69-72,'IE',75-78 10es: DDBJ:J04700; NID:	J. Biol. Chem. 264, 6404-6411, 1989 A;Title: Tandemly reiterated negative enhan A;Reference number: A33529; MUID:89197947; A:Accession: A33529	A; Molecule type: mRNA; protein A; Melecule type: mRNA; protein A; Residues: 1-210, 'I', 212-394, 'D', 396-445, 'I', 447-700 <ima> A; Residues: 1-210, 'I', 212-394, 'D', 396-445, 'I', 447-700 <ima> A; Cross-references: GB:M33254; NID:9511636; PIDN:AAA35645.1 A; Note: parts of this Samuel et emined by protein s B:Hata A: Ohno S: Akita V: Samuel E</ima></ima>	A; Molecule type: mRNA A; Residues: 1-700 <sor> R: Imajoh, S.; Aoki, K.; Ohno, S.; Emori, Y Biochemistry 27, 8122-8128, 1988 A; Title: Molecular cloning of the cDNA for A; Reference number: A31218; MUID:89166474; A; Accession: A31218</sor>	RESULT 1 CIHUH2 CALPAIN (EC 3.4.22.17) large chain 2 - human NyAlternate names: calpain chain L-2; calpain II cataly C;Species: Homo sapiens (man) C;Date: 21 Nov-1993 #sequence_revision 09-Aug-1997 #tex C;Accession: S10590; A31218; A33529 R;Sorimachi, H; Ohmi, S.; Emori, Y.; Kawasaki, H.; Sai, Biol. Chem. Hoppe-Seyler 371(Suppl.), 171-176, 1990 Biol. Chem. Hoppe-Seyler 371(Suppl.), 171-176, 1990 A;Title: A novel member of the calcium-dependent cystein A;Reference number: S10589; MUID:90380278; PMID:2400579 A;Accession: S10590
Asn #status predicted	572-604/Domain: calmodulin repeat homology <ef2> 605-634/Domain: calmodulin repeat homology <ef3> 605-634/Domain: calmodulin repeat homology <ef3> 637-669/Domain: calmodulin repeat homology <ef4> 2/Modified site: acetylated amino end (Ala) (in mature form)</ef4></ef3></ef3></ef2>	F;2-700/Product: calpain large chain 2 #status predicted <maty <calp="" calpain="" catalytic="" domain="" domain:="" f;75-327="" homology=""> F;529-560/Domain: calmodulin repeat homology <efi></efi></maty>	A;Description: catalyzes the hydolysis of peptides A;Note: cleaves preferentially after tyrosine, methionine, or arginine residues and b A;Note: cleaves preferentially after tyrosine, methionine, or arginine residues and b C;Superfamily: calpain large chain; calmodine, methionine, or arginine residues and b C;Superfamily: after amino end: calcium binding: resteine profesionese FF hand: bete	114230 ind S (small) chains	A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-67,'G',69-72,'IE',75-78,'R' <hat> A;Cross-references: DDBJ:JU04700; NID:g179910; PIDN:AAA52760.1; PID:g463086 C:Gepetics:</hat>	J. Biol. Chem. 264, 6404-6411, 1989 J. Biol. Chem. 264, 6404-6411, 1989 A; Title: Tandemly reiterated negative enhancer-like elements regulate A; Reference number: A33529; MUID:89197947; PMID:2539381 A.Accession. A33529	A;Molecule type: mRNA; protein A;Molecule type: mRNA; protein A;Residues: 1-210,'I',212-394,'D',396-445,'I',447-700 <ima> A;Residues: 1-210,'I',212-394,'D',396-445,'I',447-700 <ima> A;Cross-references: GB:M3254; NID:g511636; PIDN:AAAA35645.1; PID:g511637 A;Note: parts of this sequence were determined by protein sequencing; the amino end A;Note: parts of this sequence were determined by protein sequencing; the amino end</ima></ima>	A; Molecule type: mRNA A; Residues: 1-700 <sor> R; Imajoh, S.; Aoki, K.; Ohno, S.; Emori, Y.; Kawasaki, H.; Sugihara, H.; Suzuki, K. Biochemistry 27, 8122-8128, 1988 Biochemistry 27, 8122-8128, 1988 A; Title: Molecular cloning of the cDNA for the large subunit of the high-Ca(2+)-requi A; Reference number: A31218; MUID:8916474; PMID:2852952</sor>	RESULT 1 CIHUH2 CIHUH2 Calpain (EC 3.4.22.17) large chain 2 - human N,Alternate names: calpain chain L-2; calpain II catalytic chain; high-calcium requir C;Species: Homo sapiens (man) C;Date: 21-Nov-1993 #sequence_revision 09-Aug-1997 #text_change 16-Jul-1999 C;Date: 21-Nov-1993 #sequence_revision 09-Aug-1997 #text_change 16-Jul-1999 C;Accession: S10590, A31218; A33529 R;Sorimachi, H.; Ohmi, S.; Emori, Y.; Kawasaki, H.; Saido, T.C.; Ohno, S.; Minami, Y. Biol. Chem. Hoppe-Seyler 371(Suppl.), 171-176, 1990 A;Title: A novel member of the calcium-dependent cysteine protease family. A;Reference number: S10589; MUID:90380278; PMID:2400579 A;Recession: S10590
:) #status predicted		arginine residues and b y; calpain catalytic dom		; PID:g463086	regulate transcription o	PID:g511637 Dencing; the amino end o	gihara, H.; Suzuki, K. of the high-Ca(2+)-requi	I catalytic chain; high-calcium requir 997 #text_change 16-Jul-1999 H.; Saido, T.C.; Ohno, S.; Minami, Y. 1990 . t cysteine protease family.

Query Match Best Local Similarity

99.5%;

Score 1287; DB 1; Pred. No. 5.2e-87;

Length 700;

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Calpain (EC 3.4.22.17) large chain 2 - rabbit (fragment)
N;Alternate names: calcium-activated neutral proteinase (CANP)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: A-Jan-1988 *sequence_revision 24-Jan-1988 *text_change 16-Jul-1999
C;Accession: B24815
R;Emori, Y: Kawasaki, H: Sugihara, H: Imajoh, S:; Kawashima, S:; Suzuki, I
J. Biol. Chem. 261, 9465-9471, 1986
A;Title: Isolation and sequence analyses of cDNA clones for the large subunit A;Reference number: A92594; MUID:86250902; PMID:2424911
A;Accession: B24815
A;Molecule type: mRNA
A;Residues: 1-422 CEMO>
A;Cross-references: GB:M13797; NID:g165665; PIDN:AAA31455.1; PID:g165666
C;Superfamily: calpain large chain; calmodulin repeat homology cEF1>
F;251-282/Domain: calmodulin repeat homology cEF2>
F;327-336/Domain: calmodulin repeat homology cEF3>
F;357-391/Domain: calmodulin repeat homology cEF3>
F;359-391/Domain: calmodulin repeat homology cEF3>
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Calpain (EC 3.4.22.17) large chain 2 - chicken
N;Alternate names: m-calpain heavy chain
C;Species: Gallus gallus (chicken)
C;Date: 28-Oct-1995 **sequence_revision 03-Nov-1995 **text_change 20-Jun-2000
C;Accession: S57194
R;Sorimachi, H.; Tsukahara, T.; Okada-Ban, M.; Sugita, H.; Ishiura, S.; Suzuki,
Biochim. Biophys. Acta 1261, 381-393, 1995
A;Title: Identification of a third ubiquitous calpain species - chicken muscle
A;Reference number: S57194; MUID:95260862; PMID:7742367
A;Accession: S57194
A;Status: preliminary
A;Accession: S57194
A;Cross-references: EMBL:D38026; NID:g882068; PIDN:BAA07228.1; PID:g882069
A;Cross-references: EMBL:D38026; NID:g882068; PIDN:BAA07228.1; PID:g882069
C;Keywords: cysteine proteinase; EF hand; hydrolase
F;75-327/Domain: calpain catalytic domain homology <CALP>
F;529-560/Domain: calmodulin repeat homology <EFI>
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change 22-J
C;Accession: S38361; S08650; S39751
R;DeLuca, C.I.; Davies, P.L.; Samis, J.A.; Elce, J.S.
Biochim. Biophys. Acta 1216, 81-93, 1993
A;Title: Molecular cloning and bacterial expression of cDNA for rat
A;Reference number: S38361; MUID:94032492; PMID:8218419
A;Cross-references: EMBL:L09120; NID:94032492; PMID:8218419
A;Residues: 1-700 < DEL>
A;Cross-references: EMBL:L09120; NID:94032492; PMID:8218419
A;Residues: 1-700 < DEL>
A;Cross-references: EMBL:L09120; NID:94032492; PMID:8218419
A;Residues: 1-700 < DEL>
A;Cross-references: EMBL:L09120; NID:9402665; PIDN:AAA16327.1; PID:9
R;Samis, J.A.; Back, D.W.; Graham, E.J.; Elice, J.S.
submitted to the EMBL Data Library, February 1990
A;Reference number: S08650
A;Reference number: S08650
A;Reference number: S08650
A;References: EMBL:X31772
C;Superfamily: calpain large chain; calmodulin repeat homology calpain calpain calmodulin repeat homology calpain calpain calmodulin repeat homology calpain calmodulin ca
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92.4%; Pred.
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EF hand; heterodimer;
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A;Note: cleaves preferentially after tyrosine, methionine, or arginine residues and before the process of the p
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A;Reference number: A91354; MUID:86082358; PMID:3000828
A;Contents: annotation; gene structure
C;Comment: This calpain has calcium requirements intermediate between
C;Genetics:
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F; 637-
F; 670-
F; 105,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X01415; NID:g63332; PIDN:CAA25658.1; R;Emori, Y.; Ohno, S.; Tobita, M.; Suzuki, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-705 < OHN>
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                                             58;
                                       Score 799.5;
Pred. No. 3.5e
58; Mismatches
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Pred. No. 6.
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5.9e-70;
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J. Biol. Chem. 261 044
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F; 256-288/Domain:
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Best Local S
Matches 138
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A,Note: sequence was deduced from composition by homology C;Superfamily: calpain large chain; calmodulin repeat home C;Keywords: blocked amino end; calcium binding; cysteine I F;148-179/Domain: calmodulin repeat homology <EF1>F;191-223/Domain: calmodulin repeat homology <EF2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Separation of peptides on the basis of the difference A;Reference number: A41418; MUID:88032960; PMID:3667575 A;Accession: A41418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 19-320 < EMO>
A; Cross-references: GB:M13363; NID:g165667;
R; Kawasaki, H; Imajoh, S; Suzuki, K.
J. Biochem. 102, 393-400, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           calpain (EC 3.4.22.17) large chain 1 - rabbit (fragments)
N;Alternate names: calcium-activated neutral proteinase (CANP)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 24-Jan-1988 #sequence_revision 24-Feb-1994 #text_change
C;Accession: A24815; A41418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: Isolation and sequence analyses of cDNA clones A; Reference number: A92594; MUID:86250902; PMID:2424911 A; Accession: A24815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Residues: 1-18;125-154;313-320 < KAW>
                                                                                                                                                                                                                                                                          KALEEAGFKMPCQLHQVIVARFADDQLIIDFDNFVRCLVRLETLFKIFKQLDPENTGTIE
|:| ||||: :|::: | :||||| |||||::: | :
MAIESAGFKLNKKLYELIITRYSEPDLAVDFDNEVCCLVRLETMFRFFKTLDTDLDGVVT
                                                                                                                SDGFSIETCKIMVDMLDSDGSGKLGLKEFYILWTKIQKYQKIYREIDVDRSGTMNSYEMR
                                                                                                                                                                                    QELDDQIQANLPDEQVLSAEEIDENFKALFRQLAGEDLEISVRELQTILNRITSKHKDLR
                                                                                                                                                                                                            QAVDDEIEANL-EEFDISEDDIDDGFRRLFAQLAGEDAEISAFELQTILRRVLAKRQDIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ki, H.; Sugihara, H.; Imajoh, S.; Kawashima, 9465-9471, 1986
                                                                                                                                                                                                                                                                                                                                                                                           58.7%;
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Pred.
                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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No. 1.2e-48;
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duplication;
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C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 08-Dec-2000
C;Accession: A26213; A36740; S10591
R;Aoki, K.; Imajoh, S.; Ohno, S.; Emori, Y.; Koike, M.; Kosaki, G.; Suzuki, K.
FEBS Lett. 205, 313-317, 1986
A;Title: Complete amino acid sequence of the large subunit of the low-Ca2+-requiring A;Reference number: A26213; MUID:86301172; PMID:3017764
A;Accession: A26213
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A;Map position: 11pter-11qter
C;Complex: heterodimer of L (large) and S (small) chains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;2-714/Product: calpain large chain 1 *status predicted <MAT>
F;2-10/Product: chemotactic factor *status experimental <CHF>
F;85-337/Domain: calpain catalytic domain homology <CALP>
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A;Title: A novel member of the calcium-dependent cysteine A;Reference number: S10589; MUID:90380278; PMID:2400579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X04366; NID:g29663; PIDN:CAA27881.1; PID:g29664
R;KUnimatsu, M.; Higashiyama, S.; Sato, K.; Ohkubo, I.; Sasaki, M.
Biophys. Res. Commun. 164, 875-882, 1989
A;Title: Calcium dependent cysteine proteinase is a precursor of a chemotactic A;Reference number: A36740; MUID:90056492; PMID:2554904
A;Accession: A36740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              calpain (EC 3.4.22.17) large chain 1 [validated] - human N; Alternate names: calpain chain L-1; calpain I catalytic chain; N; Contains: chemotactic factor
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A; Residues: 1-714 < AOK>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Superfamily: calpain large chain; calmodulin repeat homology; calpain; Reywords: acetylated amino end; calcium binding; cysteine proteinase;
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Best Local :
                                                                                                                                                                      522 VELDDQIQANLPDEQVLSEEEIDENFKALFRQLAGEDMEISVKELRTILNRIISKHKDLR
                                                                                                                                                                                                                                                                          462
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KALEEAGFKMPCQLHQVIVARFADDQLIIDFDNFVRCLVRLETLFKIFKQLDPENTGTIE
                                                                                                   SDGFSIETCKIMVDMLDSDGSGKLGLKEFYILWTKIQKYQKIYREIDVDRSGTMNSYEMR
                                                                                                                                                                                                QAVDDEIEANL-EEFDISEDDIDDGFRRLFAQLAGEDAEISAFELQTILRRVLAKRQDIK 119 :||:||:||:||:|:::
                                                                       TKGFSLESCRSMVNLMDRDGNGKLGLVEFNILWNRIRNYLSIFRKFDLDKSGSMSAYEMR
                                                                                                                                                                                                                                                                       RDFFLANASRARSEQFINLREVSTRFRLPPGEYVVVPSTFEPNKEGDFVLRFFSEKSAGT
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55.5%;
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'; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                 calpain (EC 3.4.22.17) large chain 2, tissue-specific - C;Species: Rattus norvegicus (Norway rat) C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #texi
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                                           A; Note: sequence extracted from A; Accession: B48764
                                                                                         A;Cross-references: GB:D14479; NID:g441199; PIDN:BAA03370.1; A;Experimental source: stomach
                                                                                                                                            A; Molecule type: DNA; p
A; Residues: 1-703 <SOR>
                                                                                                                                                                                             A; Status: preliminary
                                                                                                                                                                                                                    J. Biol. Chem. 268, 19476-19482, 1993
A;Title: A novel tissue-specific calpain species expressed A;Reference number: A48764; MUID:93374936; PMID:7690035
A;Accession: A48764
                                                                                                                                                                                                                                                                                                 R;Sorimachi, H.;
J. Biol. Chem. 2
                                                                                                                                                                                                                                                                                                                                          C; Accession: A48764; B48764
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A; Residues: 1-586 <SOR>
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268, 19476-19482, 1993
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NCBI

backbone (NCBIN:137770,

NCBIP:137771) PID:g441200 18-Nov-1994 #text_change

20-Jun-2000

predominantly in the stoma

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C;Accession: S57195
R;Sorimachi, H.; Tsukahara, T.; Okada-Ban, M.; Sugita, H.; Ish
R;Sorimachi, H.; Tsukahara, T.; Okada-Ban, M.; Sugita, H.; Ish
Biochim. Biophys. Acta 1261, 381-393, 1995
A;Title: Identification of a third ubiquitous calpain species
A;Reference number: S57194; MUID:95260862; PMID:7742367
A;Accession: S57195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      calpain (EC 3.4.22.17) large chain 1 - chicken (fragment)
w;Alternate names: mu-calpain heavy chain
c;Specles: Gallus gallus (chicken)
C;Date: 28-Oct-1995 #sequence_revision 10-Nov-1995 #text_change
C;Accession: S57195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:D38027; NID:g882070; PID:g882071 C;Superfamily: calpain large chain; calmodulin repeat home C;Keywords: cysteine proteinase; EF hand; hydrolase F;1-208/Domain: calpain catalytic domain homology (fragme) F;457-489/Domain: calmodulin repeat homology <EF1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Keywords: cysteine proteinase; EF hand; hydrolase;1-208/Domain: calpain catalytic domain homology (fragment) <CALP>;457-489/Domain: calmodulin repeat homology <EF1>
                                     180 KALEEAGFKMPCQLHQVIVARFADDQLIIDFDNFVRCLVRLETLFKIFKQLDPENTGTIE 239
                                                                                                                                                                                                                                                                                         394 EEMVDKIEAKLPDEKVVSEGEIDENFKALFRQLAGPDMEISVTELQTILNRIIAKHKDLR
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                                                                                                                                                                                                                                                                                                                               QAVDDEIEANL-EEFDISEDDIDDGFRRLFAQLAGEDAEISAFELQTILRRVLAKRQDIK 119
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MALEASSYKLTQKLHQLLITPYTEPDLAIDFDSFVCCLVRLETMFRFFQAMDGENDGVVT
                                                                                                                                            TKGFSLESCRSMVNLMDKDGNGKLGLVEFNVLWNRIRNYLSVFRKFDLDKSGSMSAYEMR
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53.8%;
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Pred. No. 7.3e
59; Mismatches
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7.3e-47;
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R;Sorimachi, H.; Tsukahara, T.; Okada-Ban, M.; Sugita, H.; Isl Blochim. Blophys. Acta 1261, 381-393, 1995
A;Title: Identification of a third ubiquitous calpain species A;Reference number: S57194; MUID:95260862; PMID:7742367
A;Accession: S57196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 calpain (EC 3.4.22.17) large chain 3 - chicken
N;Alternate names: calpain p94 heavy chain; n-calpain-1 heavy chain
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: S57196
R;Sorimachi, H.; Tsukahara, T.; Okada-Ban, M.; Sugita, H.; Ishiura, S.; Suzi
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F;532-563/Domain: calmodulin repeat homology <EF1>
F;537-5607/Domain: calmodulin repeat homology <EF2>
F;640-672/Domain: calmodulin repeat homology <EF3>
F;105,262,286/Active site: Cys, His, Asn #status predicted
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A;Cross-references: GB:D14480; NID:g441201; PIDN:BAA03371.1; PID:g495223
A;Experimental source: stomach
A;Note: sequence extracted from NCBI backbone (NCBIN:137773, NCBIP:137775)
C;Superfamily: calpain large chain; calmodulin repeat homology; calpain catalytic C;Keywords: alternative splicing; cysteine proteinase; EF hand; hydrolase
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A;Residues: 1-810 <SOR-
A;Cross-references: EMBL:D38028; NID:g882072; PIDN:BAA07230.1; PID:g1552167
A;Cross-references: EMBL:D38028; NID:g882072; PIDN:BAA07230.1; PID:g1552167
C;Superfamily: calpain large chain; calmodulin repeat homology; calpain cat
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Best Local
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EKSEEETQFRNIFRQIAGDDMEICREELRNVLNNVVKKHKDLKTEGFELESSRSMIALMD
                                                                                      EEVENMTEADRPSKKKKGKPIIFVSDRANSNKELTTDEDAGKDGEKTHVDEKKRSSAKAR
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Pred. No. 2.1e
55; Mismatches
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Pred. No. 5.6e-39;
4; Mismatches 70
                                                                                                                               -EEFDISEDDIDDG--
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                                                                                                                                                                                                                                                                                    DB 1;
.1e-37;
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A;Cross-references: GDB:L19751; OMIM:114240;
A;Map position: 15pter-15qter
A;Note: defects in this gene can cause limb of C;Complex: heterodimer of L (large) and S (sn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J.A.; Fardeau, M.; Jackson, C. Cell 81, 27-40, 1995
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C; Function:
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A; Residues: 1-821 <RIC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
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                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                                                                                                        al Similarity
116; Conserv
                                                                                                                                                                                                                                                                                                                                                                                             47.4%;
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C;Species: Homo sapiens (man)
C;Date: 28-Apr_1995 #sequence_revision 09-Aug-1997 #text_change 16-Jul-1999
                                                                                                                           calpain (EC 3.4.22.17) large chain 3 - human N;Alternate names: calpain chain L-3; calpain III catalytic chain; muscle specific,
                                                                                                                                                                                                                                                                                                                                                                                                           SDGSGKLGLKEFYILWTKIQKYQKIYREIDVDRSGTMNSYEMRKALEEAGFKMPCQLHQV
                                                                                                                                                                                                                                                                                ITMRYADKNMNIDFDSFICCFVRLDAMFRAFHAFDKDGDGIIKLNVLEWL
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Allamand,
son, C.E.; (
Cohen,
  Fougerousse, F.
n, D.; Beckmann,
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     ч
  Chiannilkulchai,
J.S.
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                          Bourg
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A; Title: Mutations in the proteolytic enzyme calpain 3 A; Reference number: A56218; MUID:95236448; PMID:7720071 A; Status: not compared with conceptual translation 3 cause limb-girdle muscular Minami, Υ.;

A;Cross-references: GB:X85030; NID:g791039; PIDN:CAA59403.1; PID:g791040 R;Sorinachi, H.; Imajoh-Ohmi, S.; Emori, Y.; Kawasaki, H.; Ohno, S.; Mina J. Biol. Chem. 264, 20106-2011, 1989 A;Title: Molecular cloning of a novel mammalian calcium-dependent proteat A;Reference number: A94688; MUID:90062125; PMID:2555341 A;Accession: A34488 alian calcium-dependent protease PMID:2555341

A; Molecule type: mRNA A; Residues: 44-445, 'AA',448-458, 'P',460-461,'P',463-484,'T' OMIM: 253600 ,486-821

dystrophy

A;Description: catalyzes the hydolysis of peptides A;Note: cleaves preferentially after tyrosine, met nb girdle muscular (small) chains methionine, or arginine residues catalytic

C;Superfamily: calpain large chain; calmodulin repeat homology; calpain catalyte C;Keywords: calcium binding; cysteine proteinase; EF hand; hydrolase; muscular E;99-267,323-400/Domain: calpain catalytic domain homology #status atypical <CA E;649-680/Domain: calmodulin repeat homology <EF1>F:692-724/Domain: calmodulin repeat homology <EF2>F;725-754/Domain: calmodulin repeat homology <EF2>F;725-754/Domain: calmodulin repeat homology <EF2>F;757-789/Domain: calmodulin repeat homology <EF5>F;790-821/Domain: calmodulin repeat homology <EF5>F;790-821/Domain: calmodulin repeat homology <EF5>F;190-821/Domain: calmodulin repeat homology <EF5>F;190-821/Domain: calmodulin repeat homology <EF5>F;129,334,358/Active site: Cys, His, Asn #status predicted

Score 613; DE Pred. No. 2.2e 56; Mismatches

DB 1; .2e-37;

Length

821;

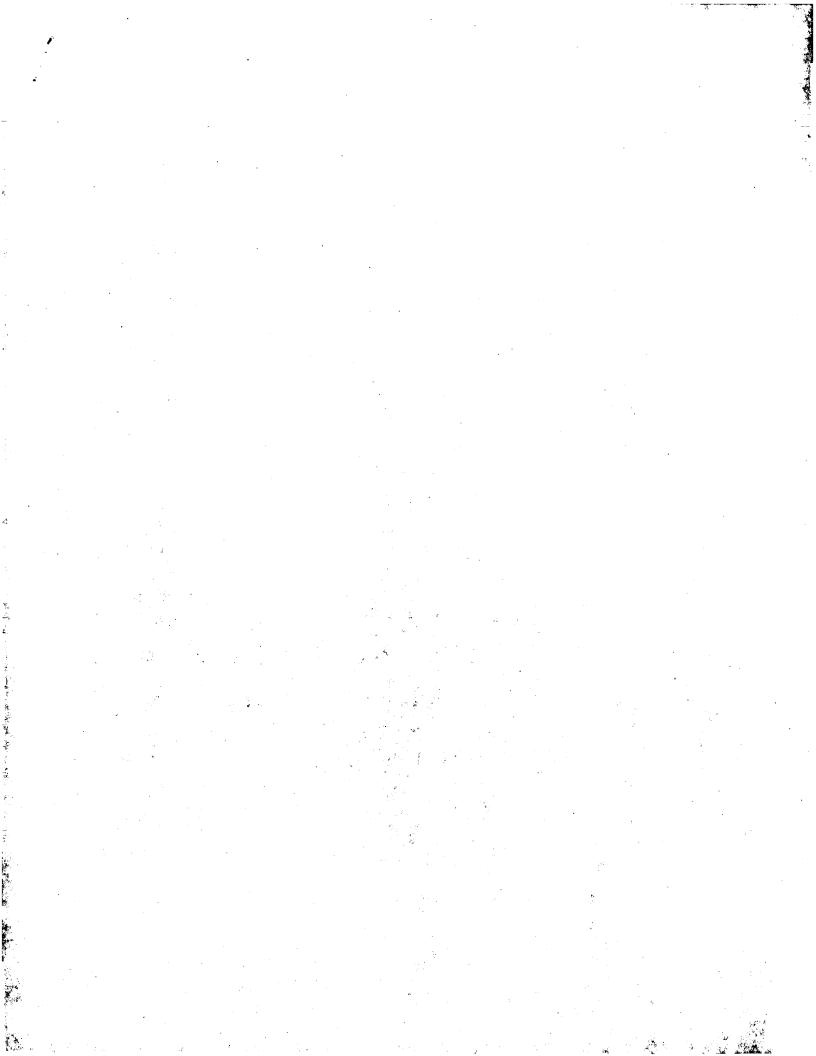
PC 19	132 VDMLDSDGSGKLGLKEFYILWTKIQKYQKIYREIDVDRSGTMNSYEMRKALEEAGFKMPC 191	Qy
SM 70	641 PGSSDQESEEQQQFRNIFKQIAGDDMEICADELKKVLNTVVNKHKDLKTHGFTLESCRSM 700	Db
IM 13	85FRRLFAQLAGEDAEISAFELQTILRRVLAKRQDIKSDGFSIETCKIM 131	Qy
PQ 64	582 EEVENTISVDRPVKKKKTKPIIFVSDRANSNKELGVDQES-EEGKGKTSPDKQKQSPQPQ 640	· Db
84		Qy
LS 581	522 KDFFLYNASKARSKTYINMREVSQRFRLPPSEYVIVPSTYEPHQEGEFILRVFSEKRNLS	Db
DY 60	1 KNEFLTNRARERSDTEINLREVLNREKLPPGEVILVPSTFEPNKDGDFCIRVFSEKKADY 60	Qy

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calpain (EC 3.4.22.17) light chain - bovine C;Species: Bos primigenius taurus (cattle) C;Date: 08-Jun-1990 #sequence_revision 08-JC;Accession: A34466
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C;Accession: B34488; S10589
R;Sorimachi, H.; Imajoh-Ohmi, S.; Emori
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                     J. Biol. Chem. 264, 17428-: A; Title: Identification of
                                          R;McClelland, P.; Lash, J.A.; Hathaway, D.R
J. Biol. Chem. 264, 17428-17431, 1989
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A; Residues: 1-50, 'E', 52-211, 'V', 213-252, 'K', 254-821 <502>
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A;Title: Molecular cloning of a novel mammalian calcium-dependen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   calpain (EC 3.4.22.17) large chain 3 -
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A; Residues: 1-821 <SOR>
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A;Accession: B34488
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117; Conserv
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                                                                                                                                                                                                                                                                                                                     LHQVIVAREADDQLIIDEDNEVRCLVRLETLEKIEKQLDPENTGTIELDLISWL 246
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                     17428-17431,
tion of major
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                     autolytic
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Pred. No. 4.3e-37;
0; Mismatches 69
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                     cleavage sites
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                     regulatory subunit
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F;1-54/Domain: glycine-rich <GLY>
F;94-125/Domain: calmodulin repeat homology <EF1>
F;137-169/Domain: calmodulin repeat homology <EF2>
F;137-169/Domain: calmodulin repeat homology <EF3>
F;170-199/Domain: calmodulin repeat homology <EF3>
F;202-234/Domain: calmodulin repeat homology <EF4>
F;235-266/Domain: calmodulin repeat homology <EF5>
                                                                                                                                                                                                                                                                                                                                                                                     A; Nolecule type: protein A; Molecule type: protein A; Residues: 2-56;125-143;157-177;247-248;250-256;265-266 A; Residues: heterodimer of L (large) and S (small) chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Sakihama, T.; Kakidani, H.; Zenita, K.; Yumoto, N.; Kikuchi, T.; Sasaki, T
Proc. Natl. Acad. Sci. U.S.A. 82, 6075-6079, 1985
A;Title: A putative Ca2+-binding protein: structure of the light subunit of A;Reference number: A25166; MUID:85298299; PMID:2994060
A;Accession: A25166
                                                                                                                                                                                                                                                                         A; Description: catalyzes the hydolysis of peptides A; Note: cleaves preferentially after tyrosine, met) C; Superfamily: calpain small chain; calmodulin rep; C; Keywords: acetylated amino end; calcium binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                calpain (EC 3.4.22.17) small chain - pig
N;Alternate names: calcium-activated neutral proteinase (CANP); calpain light
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Jul-1999
                                                                                                 F;1/Modified site: acetylated amino
                                                                                                                                                                                                                                                                                                                                                                                  C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references:
A;Accession: B25166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-266 < SAK>
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C;Superfamily: calpain small chain; calmodulin repeat homology
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Matches 88
                  Query Match
Best Local
  Matches
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                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGTMNSYEMRKALEEAGFKMPCQLHQVIVARFADDQLIIDFDNFVRCLVRLETLFKIFKQ 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISAISEAAAQYNPEPVPPRTHYSNIEANESEEVRQFRRLFAQLAGDDMEVSATELMNILN 120
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calmodulin repeat homology <EF2>
calmodulin repeat homology <EF3>
calmodulin repeat homology <EF4>
calmodulin repeat homology <EF5>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GB:M11778; NID:g164402; PIDN:AAA31010.1;
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                       35.9%;
45.2%;
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  40;
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Pred. No. 4.3e
); Mismatches
                                                 Score
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                       465; DB 1;
No. 4.3e-27;
                                                                                                                                                                                                                                                                                                        repeat
                                                                                                                                                                                                                                                                                                                             methionine,
  68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 263
                                                                                                   experimental
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  Indels
                                                                                                                                                                                                                                                                                                                                or arginine
                                                                                                                                                                                                                                                                              proteinase;
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IRVFSEKKADYQAVDDEIEANLEEFDISEDDIDDGFRRLFAQLAGEDAEISAFELQTILR 109

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A;Description: catalyzes the hydolysis of peptides
A;Description: catalyzes the hydolysis of peptides
A;Note: cleaves preferentially after tyrosine, methionine, or arginine residues and befc
C;Superfamily: calapain small chain; catanodulin repeat homology
C;KeyWords: calcium binding; cysteine proteinase; duplication; EF hand; heterodimer; hyd
F;1-54/Domain: glycine-rich <GLY>
F;94-125/Domain: calmodulin repeat homology <EF1>
F;137-169/Domain: calmodulin repeat homology <EF3>
F;170-199/Domain: calmodulin repeat homology <EF3>
F;202-234/Domain: calmodulin repeat homology <EF4>
F;235-266/Domain: calmodulin repeat homology <EF5>
                                                                                                                                                                                                                     Qγ
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R;Emori, Y.; Kawasaki, H.; Imajoh, S.; Kawashima, S.; Suzuki, K.
J. Biol. Chem. 261, 9472-9476, 1986
A;Title: Isolation and sequence analysis of cDNA clones for the A;Reference number: A24816; MUID:86250903; PMID:3013892
A;Accession: A24816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  calpain (EC 3.4.22.17) small chain - rabbit N;Alternate names: calcium-activated neutral proteinase (CANP); calpain light chain; cal C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
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Search completed: July 24, 2003, 12:53:46 Job time: 14.3158 secs
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C;Complex: heterodimer of L (large) and S (small) chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-266 < EMO>
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Best Local S
Matches 88
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                                                                                                                                                                                                                                                                                                                                                            64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KVVTRHPDLKTDGFGIDTCRSMVAVMDSDTTGKLGFEEFKYLWNNIKKWQAIYKQFDVDR 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RVLAKRQDIKSDGFSIETCKIMVDMLDSDGSGKLGLKEFYILWTKIQKYQKIYREIDVDR 169
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44.7%; Pred. No. 8.5e-27;
attive 41; Mismatches 68
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Result
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Maximum Match 100%
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Match
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1294
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Copyright (c) 1993 - 2003 Compus
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1 US-10-038-557A-9
1 US-10-038-557A-9
15 US-10-016-519-12
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15 US-10-116-519-8
16 US-09-768-877-27
17 US-09-768-877-27
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   Sequence 6, Appli
Sequence 8, Appli
Sequence 23, Appli
Sequence 23, Appli
Sequence 7, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 221, Appli
Sequence 221, Appli
Sequence 22, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 27, Appli
Sequence 27, Appli
                                                                                                                                                                                                                                                     Description
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45	44		42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
	185.5		•						•	•		•		185.5	185.5	188	191	225.5	N 1	232	234	240	465	470	in	597.5	10	613	613
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284	284	284	284	284	284	284	284	284	284	284	284	284	284	284	284	74	669	697	694	92	217	198	207	123	690	690	664	821	821
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-063-502-6	-10-18	-10-180-552-2	-10-176-913-2	-176-757-2	-10-176-482-2	-10-175-752-2	-175-738-2	-10-173-706-2	-10-063-616-6	-10-175-737	-10-176-758-2	-174-590-2	-10-063-547	-10-052-586-2	-10-006-867-6	-10-177	-09-962	-10-116-519-5	-10-116	-10-106-698-	US-09-919-039-64	US-09-981-353-138	US-09-925-301-1001	US-09-925-297-527	US-10-116-519-13	US-09-768-877-28	US-10-325-881-70	US-10-116-519-7	0 US-09-768-877-24
e 62	Sequence 236, App	e 23	23	23	e 23	e 23	e 23	23	62	e 23	23	23	62	23	62	49	Ņ	56	54,	512	Sequence 64, Appl	138	1001	527	13	28	70,	Sequence 7, Appli	Sequence 24, Appl

ALIGNMENTS

RESULT 1

Sequence 8, Application US/09840707A

Patent No. US20020077276A1

GENERAL INFORMATION:
APPLICANT: Fredeking, Terry M.
APPLICANT: Fredeking, Terry M.
APPLICANT: Ignatyev, George M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING HEMORRHAGIC VIRUS
TITLE OF INVENTION: INFECTIONS AND OTHER DISORDERS
FILE REFERENCE: 24881-301C
CURRENT APPLICATION NUMBER: US/09/840,707A
CURRENT APPLICATION NUMBER: US/99/840,707A
CURRENT FILING DATE: 2000-04-23
PRIOR APPLICATION NUMBER: 09/562,979
PRIOR APPLICATION NUMBER: 60/198,210
PRIOR APPLICATION NUMBER: 60/198,210
PRIOR FILING DATE: 1999-04-27
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 8
LENGTH: 251 В Š US-09-840-707A-8 US-09-840-707A-8 Matches Query Match Best Local OTHER INFORMATION: IL-1 receptor intracellular ligand protein OTHER INFORMATION: comprising amino acid sequence PUBLICATION INFORMATION: PATENT DOCUMENT UNMBER: 5,817,476 PATENT FILING DATE: 1995-06-07 PUBLICATION DATE: 1998-10-06 TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: 251; 1 KNFFLTNRARERSDTFINLREVLNRFKLPPGEYILVPSTFEPNKDGDFCIRVFSEKKADY Similarity KNFFLTNRARERSDTFINLREVLNRFKLPPGEYILVPSTFEPNKDGDFCIRVFSEKKADY Conservative 100.0%; 0; Score 1294; DB 9; Pred. No. 1.7e-124; ; Mismatches 0; Length 251; Indels 0; 60 60

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                                                                                                                                                  ; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-884-319-6
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US-09-884-319-6
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Best Local Similarity
Matches 251; Conserv
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                                                                                                                                                                                                                                                                               TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
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APPLICATION NUMBER: US/09/083,516
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: 08/487,942
                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: GI5258 TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSEE: LEGAL AFFAIRS, GENETICS INSTITUTE, INC
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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 ALEEAGFKMPCQLHQVIVARFADDQLIIDFDNFVRCLVRLETLFKIFKQLDPENTGTIEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                         Score 1294; DB 11;
Pred. No. 1.7e-124;
Mismatches 0;
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US-10-038-557A-8
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LENGTH: 251
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/562,979
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/198,210
PRIOR FILING DATE: 1999-04-27
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
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CURRENT FILING DATE: 2002-06-05
PRIOR APPLICATION NUMBER: 09/840,707
PRIOR FILING DATE: 2001-04-23
PRIOR FILING DATE: 2001-04-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 PUBLICATION DATE: 1998-10-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PATENT DOCUMENT NUMBER: 5,817,476
PATENT FILING DATE: 1995-06-07
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                                                   121 DGFSIETCKIMVDMLDSDGSGKLGLKEFYILWTKIQKYQKIYREIDVDRSGTMNSYEMRK 180
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US-09-768-877-23
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US-09-840-707A-9
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                                                                                                                                                        GENERAL INFORMATION
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                                                                                                                                                                        Patent No.
                                                                                                                                                                                      Sequence 23,
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                                                  APPLICANT:
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PATENT FILING DATE: 1995-06-07
PUBLICATION DATE: 1998-10-06
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PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/198,210
PRIOR FILING DATE: 1999-04-27
NUMBER OF SEQ ID NOS: 26
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APPLICANT: Ignatyev, George M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: IMPECTIONS AND OTHER DISORDERS
FILE REFERENCE: 24881-301C
                                                                                APPLICANT: POLONSKY, KENNETH S.
APPLICANT: HORIKAWA, YUKIO
APPLICANT: ODA, NAOHISA
APPLICANT: COX, NANCY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/840,707A CURRENT FILING DATE: 2001-04-23
                   APPLICANT:
                                     APPLICANT:
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OTANI, KENICHI
HANIS, CRAIG L.
BELL, GRAEME I.
                                                                                                                                                                                      Application US/09768877
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ZHOU, YUN-PING
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99.6%;
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Pred. No. 3.7e-123;
0; Mismatches 1;
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US-09-768-877-23
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Best Local Similarity
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CURRENT FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 09/422,869
PRIOR EILING DATE: 1999-10-21
NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES FILE REFERENCE: ARCD:307
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TYPE: PRT
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                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/884,319

FILING DATE: 18-Tun-2001
CLASSLEICATION: <UNKnown>
PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Graham, James
TITLE OF INVENTION: NOVEL INTERLEUKIN-1 RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lin,
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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                                                           APPLICATION NUMBER: US/09/083,516 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 02140
                                                                                                                                                                                                                                                                                                                                                        CITY: Cambridge
STATE: MA
                   APPLICATION NUMBER: 08/487,942 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: LEGAL AFFAIRS, GENETICS INSTITUTE, STREET: 87 CambridgePark Drive
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Pred. No. 3.7e-123;
""smatches 1;
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                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 09/840,707
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: 09/562,979
PRIOR APPLICATION NUMBER: 60/198,210
PRIOR FILING DATE: 1999-04-27
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/10038557A Publication No. US20030092684A1
                                                                                                                                                                                                        SEQ ID NO 9
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APPLICANT: Ignatyev, George M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS AND OTHER DISORDERS
FILE REFERENCE: 24881-301D
-10-038-557A-9
                                                                    OTHER INFORMATION: IL-1 receptor intracellular ligand protein OTHER INFORMATION: comprising amino acid sequence PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/038,557A CURRENT FILING DATE: 2002-06-05
                                                                                                                                            LENGTH: 700
TYPE: PRT
ORGANISM: Homo sapiens
               PATENT DOCUMENT NUMBER: 5,817,476
PATENT FILING DATE: 1995-06-07
PUBLICATION DATE: 1998-10-06
                                                                                                                                FEATURE:
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REFERENCE/DOCKET NUMBER: GI5258
TELECOMMUNICATION INFORMATION:
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TELEFAX: (617) 87
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STRANDEDNESS: single
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Pred. No. 3.7e-123;
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CURRENT FILING DATE: 2002-04-03
PRIOR APPLICATION NUMBER: US 60/281,253
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/288,768
PRIOR APPLICATION NUMBER: US 60/296,180
PRIOR APPLICATION NUMBER: US 60/296,180
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/300,620
PRIOR APPLICATION NUMBER: US 60/300,620
PRIOR APPLICATION NUMBER: US 60/300,620
PRIOR FILING DATE: 2001-06-25
                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.0
SEQ ID NO 12
LENGTH: 700
TYPE: PRT
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Best Local Similarity
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Best Local
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TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL CYSTEINE PROTEASE OF
TITLE OF INVENTION: SUPERFAMILY, CAN-12 AND VARIANTS THEREOF
FILE REFERENCE: D0124 NP
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              ALEEAGFKMPCQLHQVIVARFADDQLIIDFDNFVRCLVRLETLFKIFKQLDPENTGTIEL
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US-10-116-519-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
US-10-043-487-221
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SEQ ID NO 221
LENGTH: 206
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                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/10116519
Publication No. US20030114373A1
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                                     SOFTWARE: PatentIn version 3.0
SEQ ID NO 8
LENGTH: 713
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FILE REFERENCE: B4778A

CURRENT APPLICATION NUMBER: US/10/043,487

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/261,130

PRIOR APPLICATION DATE: 2001-01-12

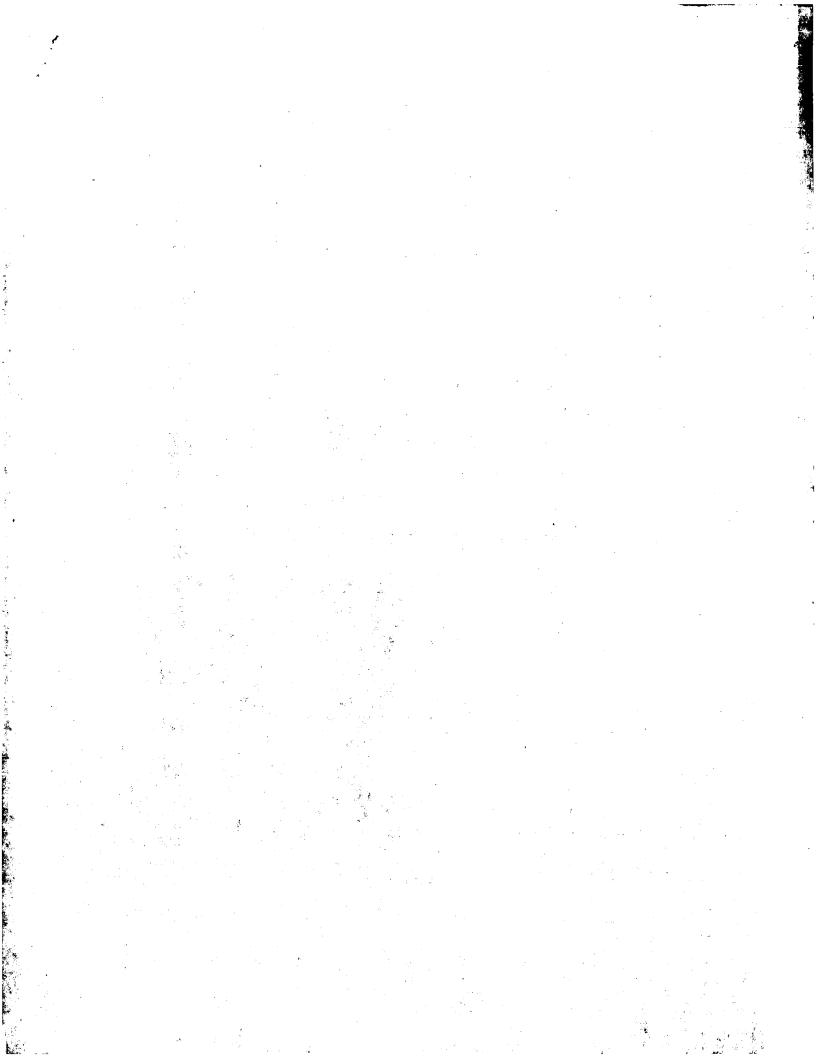
NUMBER OF SEQ ID NOS: 561
                                                                                                                                                                                                                                                                                                                     APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL CYSTEINE PROTEASE OF THE CALPAIN
TITLE OF INVENTION: SUPERFAMILY, CAN-12 AND VARIANTS THEREOF
                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/116,519
CURRENT FILING DATE: 2002-04-03
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                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/281,253
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/288,768
PRIOR FILING DATE: 2001-05-04
                                                                                                           PRIOR APPLICATION NUMBER: US 60/300,620 PRIOR FILING DATE: 2001-06-25
                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/296,180 PRIOR FILING DATE: 2001-06-06
                                                                                                                                                                                                                                                                                                         FILE REFERENCE: D0124 NP
                                                                                               NUMBER OF SEQ ID NOS: 145
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                       PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 IFKQLDPENTGTIELDLISWLCFSVL 206
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Pred. No. 1e-99;
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US-09-768-877-22
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Patent No. US20020150896A1
GENERAL INFORMATION:
APPLICANT: POLONSKY, KENNETH S.
APPLICANT: HORIKAWA, YUKIO
                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn Ver
SEQ ID NO 22
LENGTH: 714
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Best Local Similarity
Matches 137; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ZHOU, YUN-PING
APPLICANT: OTANI, KENICHI
APPLICANT: HANIS, CRAIG L.
APPLICANT: BELL, GRAEME I.
TITLE OF INVENTION: METHODS OF TREATMENT OF
FILE REFERENCE: ARCD:307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/768,877 CURRENT FILING DATE: 2001-01-23 PRIOR APPLICATION NUMBER: 09/422,869 PRIOR FILING DATE: 1999-10-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                          120 SDGFSIETCKIMVDMLDSDGSGKLGLKEFYILWTKIQKYQKIYREIDVDRSGTMNSYEMR 179
                                                                                                                                                                                                         462 RDFFLANASRARSEQFINLREVSTRFRLPPGEYVVVPSTFEPNKEGDFVLRFFSEKSAGT 521
                   180 KALEEAGFKMPCQLHQVIVARFADDQLIIDFDNFVRCLVRLETLFKIFKQLDPENTGTIE
                                                                                                                                                    61 QAVDDEIEANL-EEFDISEDDIDDGFRRLFAQLAGEDAEISAFELQTILRRVLAKRQDIK
                                                                                                                                                                                                                             1 KNFFLTNRARERSDTFINLREVLNRFKLPPGEYILVPSTFEPNKDGDFCIRVFSEKKADY 60
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                                                        TKGFSLESCRSMVNLMDRDGNGKLGLVEFNILWNRIRNYLSIFRKFDLDKSGSMSAYEMR
                                                                                                                                 VELDDQIQANLPDEQVLSEEEIDENFKALFRQLAGEDMEISVKELRTILNRIISKHKDLR 581
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COX, NANCY J.
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TYPE
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US-10-116-519-11
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          Sequence 11, Application US/10116519
Publication No. US20030114373A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: SUPERFAMILY, CAN-12 AND VARIANTS THEREOF
FILE REFERENCE: D0124 NP
CURRENT APPLICATION NUMBER: US/10/116,519
CURRENT FILING DATE: 2002-04-03
PRIOR APPLICATION NUMBER: US 60/281,253
PRIOR FILING DATE: 2001-04-03
PRIOR FILING DATE: 2001-04-03
PRIOR FILING DATE: 2001-04-03
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APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL CYSTEINE PROTEASE OF THE CALPAIN
TITLE OF INVENTION: SUPERFAMILY, CAN-12 AND VARIANTS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/296,180
PRIOR FILING DATE: 2001-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: D0124 NP
CURRENT APPLICATION NUMBER: US/10/116,519
CURRENT FILING DATE: 2002-04-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/300,620 PRIOR FILING DATE: 2001-06-25
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PRIOR APPLICATION NUMBER: US 60/288,768
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TYPE: PRT
ORGANISM: Homo sapiens
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137; Conserv
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; TYPE: PRT
; ORGANISM: RAT
US-09-768-877-27
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US-09-768-877-27
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PRIOR FILING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 145
SOFTWARE: PatentIn version 3.0
SEQ ID NO 11
LENGTH: 702
                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 27
LENGTH: 703
                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 09/422,869
PRIOR FILING DATE: 1999-10-21
NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/768,877.
CURRENT FILING DATE: 2001-01-23
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PRIOR APPLICATION NUMBER: US 60/296,180
PRIOR FILING DATE: 2001-06-06
                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: METHODS FILE REFERENCE: ARCD:307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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ORGANISM: Homo sapiens
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OTANI, KENICHI
HANIS, CRAIG L.
BELL, GRAEME I.
                             KNFFLTNRARERSDTFINLREVLNRFKLPPGEYILVPSTFEPNKDGDFCIRVFSEKKADY 60
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COX, NANCY J.
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Pred. No. 3.3e-56;
4; Mismatches 70;
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US-10-116-519-9
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CURRENT FILING DATE: 2002-04-03
PRIOR APPLICATION NUMBER: US 60/281,253
PRIOR FILLING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/288,768
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/296,180
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/300,620
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LENGTH: 709
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 48.2%; Score 624; DB 15; Length 70 Best Local Similarity 45.2%; Pred. No. 3.1e-55; Matches 113; Conservative 61; Mismatches 72; Indels
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SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL CYSTEINE PROTEASE OF THE CALPAIN
TITLE OF INVENTION: SUPERFAMILY, CAN-12 AND VARIANTS THEREOF
FILE REFERENCE: D0124 NP
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694 IIKLNVLEWL
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/ Match Local Simi nes 251;	LT 1 8-726-525-6 8-726-525-6 Quence 6, Applicent 0. 5789181 ENERAL INFORMATI APPLICANT: Lin APPLICANT: CIT TITLE OF INVENT OCHETS: 87 COUNTRY: Cambri STATE: MA COUNTRY: USA ZIP: 02140 COMPUTER READAB MEDIUM TYPE: COMPUTER: IB OPERATING SYS SOFTWARE: PAPLICATION N FILING DATE: CLASSIFICATION APPLICATION FILING DATE: CLASSIFICATION APPLICATION FILING DATE: CLASSIFICATION APPLICATION FILING DATE: CLASSIFICATION APPLICATION FILING DATE: CLASSIFICATION FILING DATE: ATTORNEY/AGENT NAME: ATTORNEY/AGENT MOLECULE B-726-525-6		465 457 430 430 430 185.5 185.5 185.5 110 170 170 170 171 111 111 111 111 111
rity nserv	ULT 1 08-726-525-6 equence 6. Application US/087265 atent No. 5789181 atent No. 5789181 general INFORMATION: Alb-Ling APPLICANT: Lin, Lih-Ling APPLICANT: Graham, James TITLE OF INVENTION: UTRACELL TITLE OF INVENTION: INTRACELL TITLE OF INVENTION: BINDING NUMBER OF SEQUENCES: 7 CORRESPONDENCE ADDRESS: ADDRESSEE: LEGAL AFFAIRS, G STREET: 87 CambridgePark Dr CITY: Cambridge STATE: MA COUNTRY: USA ZIP: 02140 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATION SYSTEM: PC-DOS/MS SOFTWARE: PATENTION DATA: APPLICATION NUMBER: US/08/7 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: 32,724 REGISTRATION NUMBER: 32,724 REGISTRATION NUMBER: GI TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 496-8224 TELEFAX: (617) 496-8224 TELEFAX: (617) 876-851 INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 251 maino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: protein 08-726-525-6		8888888993355 6888888993355 68888888993558339
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Graham, James
TITLE OF INVENTION: NOVEL
TITLE OF INVENTION: INTRACTION: BINDII
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,942
                                                                                                                                                                        MOLECULE TYPE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEPHONE: (617) 678-661
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CLASSIFICATION: 435
CTASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,7
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TYPE: ami
TOPOLOGY:
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Pred No. 2.2e-135;
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ZIP: 02140
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sequence 6, Application US/08726036A Patent No. 5981482
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FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
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TITLE OF INVENTION: NOVEL
TITLE OF INVENTION: INTRAC
TITLE OF INVENTION: BINDIN
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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LENGTH: 251 amino acid
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                     DGFSIETCKIMVDMLDSDGSGKLGLKEFYILWTKIQKYQKIYREIDVDRSGTMNSYEMRK 180
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ALEEAGFKMPCQLHQVIVARFADDQLIIDFDNFVRCLVRLETLFKIFKQLDPENTGTIEL
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                                                                                                                                                                                                                          Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NOVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
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                                                                                                                                                                                                                                                                                                                                                                                         NAME: Brown, Scott A. REGISTRATION NUMBER: 32,724
                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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100.0%; Pr
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Pred. No. 2.2e-135;
; Mismatches 0;
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                                                                                                                                                                                                                                                      Matches
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Best Local
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
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TELEFAX: (617) 8'
INFORMATION FOR SEQ II
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TITLE OF INVENTION:
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HYPOTHETICAL:
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CITY: C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sin
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ALEEAGFKMPCQLHQVIVARFADDQLIIDFDNFVRCLVRLETLFKIFKQLDPENTGTIEL
                  ALEEAGFKMPCQLHQVIVARFADDQLIIDFDNFVRCLVRLETLFKIFKQLDPENTGTIEL
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                      Length 700;
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690 DLISWLCFSVL 700

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US-08-487-942-7
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APPLICANT: Lin, Lih-Ling
APPLICANT: Graham, James
TITLE OF INVENTION: NOVEL
TITLE OF INVENTION: INTRAC
TITLE OF INVENTION: BINDIN
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                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 700 amino acid
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CORRESPONDENCE ADDRESS:
ADDRESSEE: LEGAL AFFAIRS, GENETICS INSTITUTE,
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: si
TOPOLOGY: linear
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Brown, Scott A. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
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   690
                            241 DLISWLCFSVL 251
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DLISWLCFSVL 700
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Pred. No. 6.3e-134;
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RESULT 8 US-09-422-869-23 Sequence 23, Application US/09422869 Patent No. 6235481
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; MOLECULE TYPE:
; HYPOTHETICAL: 1
US-08-726-036A-7
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Best Local Similarity
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APPLICANT: Graham, James
TITLE OF INVENTION: NOVEL
TITLE OF INVENTION: INTRACTION: BINDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 700 amino acid
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NAME: BIOWN, SCOTT A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: GI
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLIÇATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: UZIP: 02140
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                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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(617) 876-5851
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Pred. No. 6.3e-134;
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APPLICANT: POLONSKY, KENN
APPLICANT: HORIKAWA, YUKI
APPLICANT: ODA, NACHISA
APPLICANT: COX, NANCY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: ZHOU, YUN-PING
APPLICANT: ZHOU, YUN-PING
APPLICANT: HANIS, CRAIG L.
APPLICANT: BELL, GRAEME I.
APPLICANT: BELL, GRAEME I.
TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES
FILE REFERENCE: ARCD:307
CURRENT APPLICATION NUMBER: US/09/422,869
CURRENT FILING DATE: 1999-10-21
EARLIER APPLICATION NUMBER: 60/134,175
EARLIER FILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 30
SOFTWARDER OF SEQ ID NOS: 30
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                                                                                                                                                                                                                                         APPLICANT: Lin, Lih-Ling
APPLICANT: Graham, James
TITLE OF INVENTION: NOVEL
TITLE OF INVENTION: INTRAC
TITLE OF INVENTION: BINDIN
            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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                                                                                                                                                                        STREET:
                                                                                                                    COUNTRY:
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           SOFTWARE:
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APPLICATION DATA:
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                Version #1.25
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US-09-308-345A-46
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                                                         ; ORGANISM: mouse US-09-308-345A-46
                                                                                 NUMBER OF SEQ ID NOS: 49
SOFTWARE: WORDPERFECT V. 6.1
SEQ ID NO 46
LENGTH: 700
TYPE: PRT
Query Match
Best Local S
Matches 234
                                                                                                                                                                                                                                         Patent No. 6569665
GENERAL INFORMATION:
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Best Local
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                                                                                                                                                       APPLICANT: BOEHM, Thomas;
APPLICANT: DEAR, Neil T.
APPLICANT: DEAR, Neil T.
TITLE OF INVENTION: No. 6569665el calpains, their preparation and use
FILE REFERENCE: 0050/47576
CURRENT APPLICATION NUMBER: US/09/308,345A
CURRENT FILING DATE: 1999-05-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
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APPLICATION NUMBER:
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STRANDEDNESS: sir
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Pred. No. 6.3e-134;
 Score 1213; DB 4
pred. No. 1e-125;
9; Mismatches
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US-09-422-869-22
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                               GENERAL INFORMATION:
APPLICANT: POLONSKY, KENNETH
APPLICANT: HORIKAWA, YUKIO
APPLICANT: ODA, NAOHISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 47
LENGTH: 714
TYPE: PRT
ORGANISM: human
                                                                                                  Sequence 22, Appli
Patent No. 6235481
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: BOEHM, Thomas;
APPLICANT: DEAR, Neil T.
TITLE OF INVENTION: No. 65;
FILE REFERENCE: 0050/47576
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SREENAN, SEAMUS
          ODA, NAOHISA
COX, NANCY J.
                                                                                                                                                                                                                                                                     MAIESAGFKLNKKLYELIITRYSEPDLAVDFDNFVCCLVRLETMFRFFKTLDTDLDGVVT
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                                                                                                                                                                                                        FDLFKWL 708
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                                                                                                                 Application US/09422869
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Pred. No. 9.8e-76;
7; Mismatches 51;
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US-08-835-099A-1
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Best Local Similarity
Matches 137; Conser
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LENGTH: 714
                                                                                                                                                                                                                                                                                                                            APPLICANT: SHINTANI, YASUS
APPLICANT: NISHI, KAZNOTI
APPLICANT: KAWAMOTO, TOMOH
TITLE OF INVENTION: NOVEL
TITLE OF INVENTION: AND US
                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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CURRENT FILING DATE: 1999-10-21
EARLIER APPLICATION NUMBER: 60/134,175
EARLIER FILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin
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APPLICANT: BELL, GRAEME I.
TITLE OF INVENTION: METHODS
FILE REFERENCE: ARCD:307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ZHOU, YUN-PING APPLICANT: OTANI, KENICHI
 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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ADDRESSEE: DIKE, BRONSTEIN,
                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                           STREET: 130 W
CITY: Boston
STATE: MA
                                  CLASSIFICATION:
                                                    APPLICATION NUMBER: FILING DATE: 04-APR
                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               702
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                                                                                                                                                                                                                                                               130 Water
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                                                   UMBER: US/08/835,099A
04-APR-1997
                                                                                                                                                         Diskette
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AND USE
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: SHINTANI, Yasushi
APPLICANT: NISHI, Kaznori
APPLICANT: KAWAMOTO, Tomohiro
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                                                               SOFTWARE: FASTEEQ for Windows Version
APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL PRITTLE OF INVENTION: AND USE
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REFERENCE/DOCKET NUMBER: 47:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                     COMPUTER: IBM CON
OPERATING SYSTEM:
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                                               APPLICATION NUMBER: FILING DATE:
                                  CLASSIFICATION:
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08/835,099
                                                          US/09/157,349
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US-08-835-099A-2
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Patent No.
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CLASSIFICATION: 514

PARTICAL STATEM: DOS WINDOWS VERSION 2.

CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/835,099A

FILING DATE: 04-APR-1997

CLASSIFICATION: 514

PRIOR APPLICATION: 514
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Best Local 9
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                                                                                                                                                                                                                                                                                           APPLICANT: SHINTANI, Yasushi
APPLICANT: NISHI, Kaznori
APPLICANT: KAWAMOTO, Tomohiro
                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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REFERENCE/DOCKET NUMBER: 47:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-223-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 03-APR-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                   COUNTRY: U
ZIP: 02109
                                                                                                                                                                                   STATE:
                                                                                                                                                                                              CITY: Boston
                                                                                                                                                                                                  ADDRESSEE: Din.,
130 Water
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TOPOLOGY: li
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APPLICATION NUMBER: 9710:
APPLICATION:
O3-APR-1997
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Pred. No. 2.6e-65;
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Gaps

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; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 712 amino acids
; TYPE: amino acid
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-835-099A-2
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Search completed: July 24, 2003, 12:58:02 Job time : 12.1016 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 083649/1996
FILING DATE: 05-APR-1996
APPLICATION NUMBER: 97105508.2
FILING DATE: 03-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S
REFERENCE/DOCKET NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 47342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 617-523-6440
                                                                                                                  521 LEIGDVVAGNPYEPHPSEVDQEDDQFRRLFEKLAGKDSEITANALKILLNEAFSKRTDIK 580
                                                            701 LSLAEWLC 708
                                                                                      240 LDLISWLC 247
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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     length: 0
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1: /SIDS1/gcgdata/gei
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AAB86128
AAE25059
AAB86130
AAB6130
AAB51707
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Type I, p80 IL-1-r
Human interleukin-
Human interleukin-
Human interleukin
Human calpain 80kD
Human calpain B0kD
Human prey protein
Gene 36 human secr
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79 20 20 20 20 20 20 20 20 20 20 20 20 20	74.5 449 613 446.5 50 613 446.5 50 613 446.5 50 613 449 613 449
686 723 123 123 207 268 442 447 791 184 248 828 828 828 828 828 828 828 828 8	191 191 21 327 24 7 327 24 7 703 18 7 703 23 7 703 23 7 712 18 7 702 22 9 702 23 9 703 22 1 82 1 757 22 1 82 1 757 22 1 82 1 757 23 1 757 24 1 757 24 1 757 25 1
AAB62153 AAB62153 AAB62153 AAB454075 AAB45562 AAB415640 AAB466129 AAB66129 AAB66129 AAB661328 AAB663328 AAB663328 AAB663328 AAB663328 AAB663328 AAB663328 AAB663328 AAB663328 AAB663328 AAB663328 AAB663328 AAB663328 AAB663328 AAB663328	
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ALIGNMENTS

RESULT 1 AAW19991

	PI Graham J		XX	PR 07-JUN-1995;	XX	PF 06-MAY-1996;	XX	PD 19-DEC-1996.	XX	PN WO9640907-A1.	OS Homo sapiens.	XX ·		IL-1	IL;			DT 27-AUG-1997	XX	AC AAW19991;	XX		
Graham J, Lin L; WPI: 1997-052315/05.	(GEMY) GENETICS INST INC						996.		7-A1.	lens.		lular doma	iated resp	rleukin;	•	p80 IL-1-1			•-		standard		
		INST INC.		95US-0487942.		96WO-US06363.							ain; CANP; cal	ponse; inflam	receptor; liga	•	eceptor into	(first entry)				AAW19991 standard; Protein; 251 AA.	
												,	intracellular domain; CANP; calcium activated neutral protease.	IL-1 mediated response; inflammation; inflammatory; antibody;	interleukin; receptor; ligand; screening assay; inhibitor;	•	Type I, p80 IL-1-receptor intracellular domain liqand.					AA.	

PXX

N-PSDB; AAT71218

Interleukin-1 receptor intracellular ligand proteins and related DNA

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RESULT 2
AAB37796
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Best Local S
Matches 251
                                                                                                                                                                                                                       Human; interleukin-1; IL-1; IL-lalpha; IL-lbeta; IL-1 receptor; antiinflammatory; haemostatic; antibacterial; immunosuppressive; immunomodulator; cardiant; cytostatic; neuroprotective; respiratory; inflammation; infection; sepsis; cachexia; autoimmune disorder; cardiovascular disorder; chronic myelogenous leukaemia; multiple sclerosis; inflammatory bowel disease; Crohn's disease.
                                                                                                                                                02-NOV-2000
                                                                                                                                                                         WO200064479-A1
                                                                                                                                                                                                                                                                                                           Human interleukin-1 receptor intracellular ligand protein
                                                                                                                                                                                                                                                                                                                                  23-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                  AAB37796 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                are used to screen for agents (e.g. antibodies) that are capable of inhibiting or blocking the binding of an IL-1-R intracellular ligand to the intracellular domain of IL-1-R, i.e. inhibitors of IL-1 activity. Such agents can be used to treat inflammatory conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
 Novel
                                                                         (ANTI-) ANTIBODY SYSTEMS INC
                                                                                                                        26-APR-2000;
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                         2000-679646/66
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compositions comprising tetracycline or tetracycline-like
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            represents a protein that has interleukin-1 receptor (IL-1-R) lular ligand activity. IL-1-R intracellular ligand proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALEEAGFKMPCQLHQVIVARFADDQLIIDFDNFVRCLVRLETLFKIFKQLDPENTGTIEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QAVDDEIEANLEEFDISEDDIDDGFRRLFAQLAGEDAEISAFELQTILRRVLAKRQDIKS
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llarity 100.0%;
Conservative 0
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Pred. No. 1.1
); Mismatches
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1.1e-122;
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DLISWLCFSVL

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diseases. Such diseases include acute inflammatory conditions with viral haemorrhagic diseases (including diseases caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 responses colitis -
                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                compounds for treating and/or preventing acute inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is given in a specification compositions and methods containing tetracycline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 158-159; 183pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                compounds
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                                    181
                                                                    181
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                                DGFSIETCKIMVDMLDSDGSGKLGLKEFYILWTKIQKYQKIYREIDVDRSGTMNSYEMRK
                                                                                                                                                                                    QAVDDEIEANLEEFDISEDDIDDGFRRLFAQLAGEDAEISAFELQTILRRVLAKRQDIKS
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                                                                                                  DLISWLCFSVL
                                                                                                                                                                   QAVDDETEANLEEFDISEDDIDDGFRRLFAQLAGEDAEISAFELQTILRRVLAKRQDIKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for the treatment and/or prevention of acute inflammatory and diseases, e.g. septic shock and immune complex-induced
                                                                                                                                                                                                                                                                                                                                                                    251 AA;
                                                                                                                                                                                                                                                                                                 100.0%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                Score 1294; DB 21; Pred. No. 1.1e-122;
                                                                                                                                                                                                                                                                                                  Mismatches
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RESULT 3
AAW19992
ID AAW1
07-JUN-1995;
                                                                                                                                 Human CANP used
                                                                                                                                                                    AAW19992;
                                                                                                                                                                                    AAW19992 standard;
                                                                                                               IL; interleukin; receptor; ligand; screening assay; inhibitor;
                                                                                                                                                   27 - AUG - 1997
                                06-MAY-1996;
                                                                WO9640907-A1
                                                                                Homo sapiens
(GEMY ) GENETICS INST
                                                                                                  intracellular
                                                                                                         L-1 mediated
                                                                                                                                                  (first entry)
                                                                                                          response;
                                                                                                  domain; CANP; calcium
                               96WO-US06363
                                                                                                                                  to
                                                                                                                                 identify inhibitors of interleukin-1 activity.
                                                                                                                                                                                    Protein;
                                                                                                          inflammation;
                                                                                                                                                                                    700
                                                                                                                                                                                    AA
                                                                                                           inflammatory;
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antibody

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RESULT 4
AAB37797
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Best Local S
Matches 250
                                                                                                                    Human; Interrent and interrent antipacterial; ammunomatory; haemostatic; antibacterial; ammunomodulator; cardiant; cytostatic; neuroprotective; respiration inflammation; infection; sepsis; cachexia; autoimmune disorder; cardiovascular disorder; chronic myelogenous leukaemia; cardiovascular disorder; chronic myelogenous leukaemia; cardiovascular disorder; chronic myelogenous leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW19992 represents human calcium activated neutral protease (CANP). This protein was found to have an area of high homology with an interleukin-1 receptor (IL-1-R) intracellular ligand (encoded by cDN) clone 14w, see AAT71218) and thus will display some of the same properties of this protein. IL-1-R intracellular ligand proteins are used to screen for agents (e.g. antibodies) that are capable of inhibiting or blocking the binding of an IL-1-R intracellular ligand to the intracellular domain of IL-1-R, i.e. inhibitors of IL-1
                                                                                                       Homo
                                                                                                                                                                                                                                                                                                                                         AAB37797 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 14; Page 36-38;
              26-APR-2000; 2000WO-US11700
                                             02-NOV-2000
                                                                                                                                                                                                                                              Human
                                                                                                                                                                                                                                                                             23-FEB-2001
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- used to identify inhibitors of the proteins for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Graham J,
                                                                                                                                                                                                                                                                                                                                                                                                                       690
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                                                                                                                                                                                                                                              interleukin-1 receptor intracellular ligand protein
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                                                                                                                                                                                                              interleukin-1; IL-1; IL-1alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KNFFLTNRARERSDTFINLREVLNRFKLPPGEYILVPSTFEPNKDGDFCIRVFSEKKADY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLISWLCFSVL 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  700 AA;
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                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŗ
                                                                                                                                                                                                                                                                                                                                         Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1287; DB 18;
Pred. No. 2.3e-121;
D; Mismatches 1;
                                                                                                                                                                                 immunosuppressive;
rotective; respiratory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
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27-JUL-2001 AAB86128;

(first 80kDa

calpain

subdomain entry)

protein

fragment

AAB86128 standard;

protein; 700

ΑA

180

569 120

629

689 240 509 60

0

muscular;

antitumor

Calpain; calcium-activated cystein proteinase; human; Ca-activated cystein proteinase; protein coordinate de structure-function study; ischemic condition; muscular

muscular

n; spatial structure; data; treatment; lar dystrophy; tumor;

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AAB86128
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                                                                                                                                                                                                                                                                                        Дb
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Best Local S
Matches 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       multiple sclerosis, inflammatory responses associated with trauma, systemic inflammatory response syndrome (SIRS), adult respiratory distress syndrome (ARDS), acute liver failure, inflammatory bowel and Crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel compositions comprising tetracycline or compounds for the treatment and/or prevention responses and diseases, e.g. septic shock and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                       DLISWLCFSVL
                                                                                                                                                                                                                                      DGFSIETCKIMVDMLDSDGSGKLGLKEFYILWTKIQKYQKIYREIDVDRSGTMNSYEMRK
                                                                                                                                                                                                                                                                                      QAVDDEIEANLEEFDISEDDIDDGVRRLFAQLAGEDAEISAFELQTILRRVLAKRQDIKS
                                                                                                                                                                                                                                                                                                                                                        KNFFLTNRARERSDTFINLREVLNRFKLPPGEYILVPSTFEPNKDGDFCIRVFSEKKADY
                                                                                                                                                      ALEEAGFKMPCQLHQVIVARFADDQLIIDFDNFVRCLVRLETLFKIFKQLDPENTGTIEL
                                                                                                                                                                       ALEEAGFKMPCQLHQVIVARFADDQLIIDFDNFVRCLVRLETLFKIFKQLDPENTGTIEL
                                                                                                                                                                                                                        DGFSIETCKIMVDMLDSDGSGKLGLKEFYILWTKIQKYQKIYREIDVDRSGTMNSYEMRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        700 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 159-162; 183pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ignatyev GM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         99.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1287;
Pred. No. 2.
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2.3e-121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 700;
                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Best Local
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Human: calpain; nervous system disorder; amyotrophic lateral sclerosis; Parkinson's disease; dementia; genito-urinary system disorder; stroke; Alzheimer's disease; multiple sclerosis; benign prostate hyperplasia; urinary incontinence; gene therapy; cytostatic; nootropic; uropathic;
                                                                                                                                 Human calpain
                                                                                                                                                                                                                                                                                           AAE25059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                           standard;
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                                                                                                                                                                                                                                                                                           Protein;
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99.6%;
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2.3e-121;
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Ca-activated cystein

calpain

80kDa subdomain

protein

fragment.

(first entry)

AAB86130

standard;

protein;

700

Calpain; calcium-activated cystein proteinase; human;

proteinase; protein coordinate dat tudy; ischemic condition; muscular

n; spatial structure; data; treatmen+ dystrophy;

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RESULT 7
AAB86130
ID AAB8
XX AAB8
AC AAB8
XX AAB8
XX AAB8
XX AAB8
XX Calp
KW Calp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treating, ameliorating or correcting dysfunctions or diseases such as peripheral or central nervous system (CNS) disorders (e.g., Parkinson's disease, Alzheimer's disease, multiple sclerosis, stroke, amyotrophic lateral sclerosis, dementia) and genito-urinary system disorders such as urinary incontinence and benign prostate hyperplasia. They are also used in gene therapy. The present sequence is human calpain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human calpain polypeptide, useful for treating central nervous system disorder and genito-urinary incoluding urinary incontinence and benign prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 101-104; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encoding such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention
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                                                                                                                                                                                                                                                                            ALEEAGFKMPCQLHQVIVARFADDQLIIDFDNFVRCLVRLETLFKIFKQLDPENTGTIEL
                                                                                                                                                                                                                                                                                                                                                                                     QAVDDEIEANLEEFDISEDDIDDGFRRLFAQLAGEDAEISAFELQTILRRVLAKRQDIKS
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                                                                                                                                                                                                                                                                                                                                                                      QAVDDETEANLEEFDISEDDIDDGVRRLFAQLAGEDAEISAFELQTILRRVLAKRQDIKS
                                                                                                                                                                                                                                                                                                                                                                                                                             KNFFLTNRARERSDTFINLREVLNRFKLPPGEYILVPSTFEPNKDGDFCIRVFSEKKADY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          relates to novel human calpain proteins and polynucleotides proteins. Calpain sequences of the invention are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.5%;
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Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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RESULT 8
ABG70047
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DT 21-C
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Prey
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Matches 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes the novel spatial structure of human and rat neutral calcium-activated cystein protease (calpain) family. The spatial structure (especially crystalline forms) are used for structure-function studies, particularly for identifying (pseudo)substrates, inhibitors and activators of calpains, potentially useful for treatment of ischemic conditions, muscular dystrophy and/or tumors. The products of the invention have anti-ischemic, muscular and antitumor activity. This sequence represents the rat calpain 80kDa subunit described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spatial structures containing calpain-derived polypeptides, useful for identifying calpain modulators and substrates, potentially useful e.g. {\rm c}
                         Human prey protein
                                                                                            ABG70047 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 15; Fig 6; 182pp; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN (PROT-) PROTEROS BIOSTRUCTURES GMBH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          identifying calpain modulators antitumor agents
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                                                                                                                                                                                                                                                                                                      QAVDDEIEANLEEFDISEDDIDDGFRRLFAQLAGEDAEISAFELQTILRRVLAKRQDIKS
                                                                                                                                                    DLISWLSFSVL
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                                                                                                                                                                                                                                            DGFSIETCKIMVDMLDEDGSGKLGLKEFYILWTKIQKYQKIYREIDVDRSGTMNSYEMRK
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                                                (first
ospB; ospD1; ipaD; ipaC; ipaH9.8;
                        for Shigella ospB #6.
                                                                                            Protein;
                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                             93.5%;
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Pred. No. 1.4e-113;
1; Mismatches 8;
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The invention relates to a complex of protein-protein interactions to between a Shigella flexmeri polypeptide (e.g. ospb), ospb1, ipaC, ipaH9, 8, ospG and ospC1) and a mammalian polypeptide defined in the specification. The complexes are formed using the yeast two-hybrid system. Also included are (1) a recombinant host cell expressing the interactions between the shigella flexneri polypeptide and a mammalian polypeptide and a mammalian polypeptide defined in the specification; (2) selecting a modulating compound that inhibits or activates the protein-protein interactions; (3) a modulating compound obtained from the method of (2); (4) a SID (selected interacting domain) polypeptide or its fragment or variant comprising the human polypeptides appearing as ABG70042-ABG770242; (5) a SID polynucleotide or its fragment comprising (5); or encoding the above polypeptides a vector comprising (5) a recombinant host cell containing the vector; and (10) a protein of the interaction of the component of the vector of the component of the com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                flexneri polypeptide and a prey mammalian or human placenta for treating or preventing bacillary dysentery in a mammal of
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                                                                                                                                                                                                                     DVDRSGTMNSYEMRKALEEAGFKMPCQLHQVIVARFADDQLIIDFDNFVRCLVRLETLFK
                                                                                                                                                                                                                                                                                                                                                  TILRRVLAKRQDIKSDGFSIETCKIMVDMLDSDGSGKLGLKEFYILWTKIQKYQKIYREI
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                                                                                   IFKQLDPENTGTIELDLISWLCFSVL 251
                                                                                                                                                                           DVDRSGTMNSYEMRKALEEAGFKMPCQLHQVIVARFADDQLIIDFDNFVRCLVRLETLFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001US-261130P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.2%;
99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1051; DB 23; Pred. No. 3.6e-98; 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pracenta polypeptide mammal or human -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide mprising the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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AAB51707 standard; Protein; 191 AA

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Best Loc
Matches
                                       Query Match
                                                                                                                                                                                                                                                                                   ophthalmological. The polynucleotides and polypeptides can be used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases, hyperproliferative disorders, cardiovascular disorders, cerebrovascular disorders, anglogenesis, nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           used
                                                                                                                       increase or decrease storage capabilities. AAC93355 to AAC93363 and AAB51619 represent sequences which are used in the exemplification operant invention
                                                                                                                                                                                                           disorders, infections caused by bacteria, viruses and fungi and ocular disorders. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of
                                                                                                                                                                                                                                                                                                                                                                                                                           antiarthritic; immunosuppressive; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homologous to them, which are given in the exemplification of the prese invention. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Examples of activities include:
                                                                             Sequence
                                                                                                                                                                         primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human secreted proteins given in AAB51620 to AAB51668. AAB51669 to AAB51722 represent human secreted polypeptide sequences and protein homologous to them, which are given in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acid molecule encoding a human secreted protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-APR-1999;
20-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fungicide; ophthalmological; gene therapy; autoimmune disease; infection;
hyperproliferative disorder; cardiovascular disorder; angiogenesis;
cerebrovascular disorder; nervous system disorder; ocular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cerebroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antirheumatic; antiproliferative; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB51707;
                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polynucleotide sequences given in AAC93364 to AAC93412 encode the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 human secreted protein homologous amino acid sequence #147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000-619225/59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 secreted protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN GENOME SCI INC
ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preventing, treating or ameliorating a medical condition
                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruben SM,
                                                                           191 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0128702.
2000US-0177049.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000WO-US09069.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 skin aging; food additive; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nootropic; neuroprotective; antibacterial; virucide;
                   74.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     540pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Komatsoulis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosis; immunosuppressive; antiarthritic;
Score 969; DB 21;
Pred. No. 6.5e-90;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cardiant; vasotropic;
                                                                                                                                     exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
neuroprotective; antibacterial; virucide; fungicide; and ophthalmological. The polynucleotides and polypeptides can be used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases, hyperproliferative disorders, cardiovascular disorders, cerebrovascular disorders, anglogenesis, nervous system
                                                                                                                      and cells the genes are expressed in Examples of activities include: antiarthritic; immunosuppressive; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; noctropic; neuroprotective; antibacterial; virucide; fungicide; and
                                                                                                                                                                                     AAB51722 represent human secreted polypeptide sequences and proteins homologous to them, which are given in the exemplification of the present invention. Human secreted proteins have activities based on the tissues
                                                                                                                                                                                                                                                                                               Disclosure; Page 522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-APR-1999;
20-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-APR-2000; 2000WO-US09069.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cerebrovascular disorder; nervous system disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cerebroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted protein sequence encoded by gene 36 SEQ ID NO:148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB51708 standard; Protein; 191
                                                                                                                                                                                                                                                            The polynucleotide sequences given in AAC93364 to AAC93412
                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acid molecule encoding a human secreted protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC (ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fungicide; ophthalmological; gene therapy; autoimmune disease; infection;
hyperproliferative disorder; cardiovascular disorder; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                  2000-619225/59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    healing; skin aging;
                                                                                                                                                                                                                                          secreted proteins given
                                                                                                                                                                                                                                                                                                                             preventing, treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGFSIETCKIMVDMLDSDGSGKLGLKEFYILWTKIQKYQKIYREIDVDRSGTMNSYEMRK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DLISWLCFSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLISWLCFSVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DGFSIETCKIMVDMLDSDGSGKLGLKEFYILWTKIQKYQKIYREIDVDRSGTMNSYEMRK
                                                                                                                                                                                                                                                                                                                                                                                                                 Ruben SM,
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2000US-0177049.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nootropic; neuroprotective;
                                                                                                                                                                                                                                                                                           540pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                   Komatsoulis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      food additive; preservative.
                                                                                                                                                                                                                                                                                                                              or
F
                                                                                                                                                                                                                                            in AAB51620 to AAB51668. AAB51669
                                                                                                                                                                                                                                                                                                                             ameliorating a
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و
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibacterial; virucide;
                                                                                                                                                                                                                                                                                                                                medical condition
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                                                                                                                                                                                                                                                             encode
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                                                                        used
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RESULT 11
AAE23085
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Best Local
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                                                                                                                                                        10-JUL-2000;
27-JUL-2000;
27-JUL-2000;
27-JUL-2000;
27-JUL-2000;
07-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. AAC93355 to AAC93363 and AAB51619 represent sequences which are used in the exemplification of the complete of 
                                                                                                                                                                                                                                                                                                                                                06-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                06-JUL-2001; 2001WO-US21427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phenotype modulation;
genetic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transgenic; transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Calcium-activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE23085 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present invention.
                                                                                                                                    07 - AUG
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                                                                                                                                                                                                                                                                              10-JUL-2000;
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                                  2000US - 217449p.
2000US - 217450p.
2000US - 217660p.
2000US - 221491p.
2000US - 221669p.
2000US - 223170p.
2000US - 223172p.
2000US - 223172p.
2000US - 223172p.
2000US - 2244037p.
2000US - 244037p.
2000US - 244111p.
2001US - 301217p.
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                                                                                                                                                                                                                                                                                                                                                2000US-216251P.
2000US-216258P.
                                                                                                                                                                                                                                                                                                                                                                                                 2000US-216109P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            calcium-activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  animal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 963; DB Pred. No. 2.6e 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pharmacological therapy; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neutral protease; enzyme;
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inhibition, significant decrease in their response latency to the hot plate test or a decreased response threshold to metrazol. Agents that modulate the expression, function or activity of the target gene are useful for treating a disorder associated with a mutation in tryptase gene or in limulus clotting factor protease-like gene. The transgenic animals are useful for testing the efficacy of proposed genetic and pharmacological therapies for human genetic diseases. They are useful as models for diseases, disorders or conditions associated with pharmaceuticals, therapies and interventions which may be effective in the pharmaceuticals, therapies and interventions which may be effective in the pharmaceuticals, therapies and interventions which may be effective in the pharmaceuticals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to non-human transgenic animals preferably transgenic mice comprising disruption in target gene such as tryptase gene. The invention also relates to compositions and methods relating to the characterisation of gene functions. The transgenic animals are useful for identifying an agent that modulates the expression or function of a target. They are useful for identifying an agent that modulates a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clotting factor protease-like genes by administering an agent to t transgenic animal and determining whether the agent modulates the phenotype where the agent has effect on decreased body weight, decthymus weight, decreased thymus to body weight ratio, increased principles agent decreased the second of the se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel non-human transgenic animal, preferably transgenic mice comprising disruption in target gene, e.g., tryptase gene, us identifying an agent that modulates expression or function of
                                             treating a disease or other phenotypic characteristics of the animal. The present sequence is calcium-activated neutral protease protein. This sequence is used in the exemplification of the invention.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phenotype associated with a disruption in tryptase genes or limulus
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n of target
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RESULT 12
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                                                                                                                                                                                         TNGFSLESCRSMVNLMDRDGNGKLGLVEFNILWNRIRNYLTIFRKFDLDKSGSMSAYEMR
                                                                                                                                                                                                    SDGFSIETCKIMVDMLDSDGSGKLGLKEFYILWTKIQKYQKIYREIDVDRSGTMNSYEMR
                                                                                                                                                                                                                                  QELDDQIQANLPDEKVLSEEEIDDNFKTLFSKLAGDDMEISVKELQTILNRIISKHKDLR
                                                                                                        FDLFKWL
                                                                                                                                               MAIEAAGFKLNKKLHELIITRYSEPDLAVDFDNFVCCLVRLETMFRFFKLLDTDLDGVVT
          (first entry)
                                                                                                                           246
                                                    Protein;
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Matches Query Match

Local

al Similarity 140; Conserv

Conservative

58;

Pred. No. 2.3e B; Mismatches Score 773.5; Pred. No. 2.

.3e-69; DB 23; 48;

Indels Length

Gaps

713; 1;

59.8%; 56.7%;

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disorders; neurological disorders; gastrointestinal disorders; transport disorders; and connective tissue disorders. They may also be used to screen for modulators of protein activity or gene expression. DITHP proteins can additionally be used in analysis of the proteome of a tissue or cell type and to induce antibodies. The dithp nucleic acids are additionally useful in somatic or germline gene therapy of the disorders mentioned above, as a source of antisense sequences, as a source of probes and primers, in genotyping and identification of individuals, in probes and primers, in genotyping and identification of individuals, in
                                                                                                                                                                                                         proteins; microarrays comprising dithp nucleic acid sequences; methods of detecting dithp nucleotide and protein sequences; methods of screening for compounds which specifically bind a DITHP protein; and methods of assessing the toxicity of test compounds using a dithp hybridisation probe. Dithp nucleic acid sequences and DITHP proteins may be used in the diagnosis of a wide variety of conditions including cancer and other cell proliferative disorders; autoimmune or inflammatory disorders; bacterial, viral, fungal or parasitic infections; hormonal disorders; metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            identifying test compound which encoded by human diagnostic and induce antibodies
                                                                                                                                                                                                                                                                                                                                                                 sequences of the invention; recombinant vectors, host cells and transgenic organisms comprising a dithp nucleic acid sequence; the recombinant production of DITHP proteins; antibodies specific for DITHP
                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to novel human diagnostic and therapeutic polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded proteins (DITHP; ABR41136-ABR41812). The invention also relates to polynucleotide sequences at least 90% identical to the dithp cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 27; SEQ ID No 1058; 591pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human diagnostic and therapeutic polypeptide useful for identifying test compound which specifically binds to a polypeptide incoded by human diagnostic and therapeutic polynucleotide, and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
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29-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer; cell proliferative disords inflammatory disorder; infection; neurological disorder; gastrointes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human DITHP protein modification/maintenance
the generation of transgenic animal models of human disease or knock in
humanised animals, in toxicological testing, and in transcript imaging.
The present sequence represents a DITHP protein which is involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-MAY-2001;
17-MAY-2001;
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DB; ACC46461.
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2001US-280068P.
2001US-291280P.
2001US-291829P.
2001US-291849P.
2001US-299428P.
2001US-299776P.
2001US-300001P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENOMICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tive disorder; autoimmune disorder;
infection; hormonal disorder; metabolic disorder;
gastrointestinal disorder; transport disorder;
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Liu TF,
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SA, Chen AJ,
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O, Yap PE, Amsh
DA, Kleefeld Y,
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RESULT 13
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AC CAlpa
KW Calpa
KW Scree
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                                                                                                            Claim 1;
                                                                                                                                                               and treating cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      screening; activator; inhibitor; treatment; prevention; cancer; cerebral apoplexy; cerebral infarction; subarachhoid haemorrhage; Alzheimer's disease; myodystrophy; cataracts; collagen disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Calpain; human;
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Note: The sequence data for this patent did no specification, but was obtained in electronic
                                                                                                                                                                                              Human calpain protein and related DNA
                                                                                                                                                                                                                                                                                                                                 Kawamoto T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pages 23-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LDLISWLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KALEEAGFKMPCQLHQVIVARFADDQLIIDFDNFVRCLVRLETLFKIFKQLDPENTGTIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                 Nishi K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97EP-0105508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disease; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leukocyte; calcium dependent cysteine
vator; inhibitor; treatment; prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein; 703
                                                                                                                                                                    stroke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.78;
52.48;
                                                                                                            43pp; English
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Pred. No. 3.6e-59;
                                                                                                                                                                    etc
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format
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                                                                                                                                                                                              drug
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The present sequence is calpain, a human leukocyte derived calcium dependent cysteine protease. Calpain can be used to for compounds that activate or inhibit its proteolytic act

activity to screen

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 130;
                                                                                                                                                                                                                                                                                                    atherosclerosis; psoriasis; Alzheimer's disease; mental disorder; cancer; gastrointestinal disorder; cushing's syndrome; seizure; glaucoma; stroke; epithelial disorder; urticaria; anorexia; trauma; asthma; eczema; nausea; hypertension; neurological disorder; Parkinson's disease; drug screening; cardiant; cell proliferative disorder; multiple sclerosis; osteoporosis; diabetes mellitus; glomerulonephritis; cardiovascular disorder; anaemia; autoimmune disorder; inflammatory disorder; myocardial infarction; AIDS; developmental disorder; reproductive disorder; infertility; diarrhoea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Calpain DNA can be used to treat or prevent cancer, cere apopLexy, cerebral infarction, subarachnoid haemorrhage, Alzheimer's disease, mydystrophy, cataracts, ischaemic disease, atherosclerosis, arthritis or collagen disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human protease PRTS-3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                      Human; protease; PRTS-3; tranquilliser; gene therapy; vaccine; allergy; infection; dermatitis; arteriosclerosis; rheumatoid arthritis; hepatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE14338
 04-MAY-2000; 2000US-202082P
                            04-MAY-2001;
                                                                                                                              Domain
                                                                                                                                                           Domain
                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                        dementia; acidosis; cataract; gynaecomastia; epilepsy; jaundice
                                                                                                                                                                                      Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TALRKAGETLNSQVQQTIALRYACSKLGINFDSFVACMIRLETLFKLFSLLDEDKDGNVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KALEEAGFKMPCQLHQVIVARFADDQLIIDFDNFVRCLVRLETLFKIFKQLDPENTGTIE
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                            2001WO-US14651
                                                                                                                                                        /note=
99..11
                                                                                                                                                                                      /note=
45..34
                                                                                                                              /note=
355..5
                                                                                                                                                                                                                    Location/Qualifiers
1..508
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52.4%;
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e= "Calpain larger
                                                                                                                                                                    "Calpain
                                                                                                                                                                                                "Calpain catalytic domain"
                                                                                                                                          "Thiol protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45;
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Pred. No. 9.9e
15; Mismatches
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ches 72;
                                                                                                               subunit domain
                                                                                                                                          Cyc motif"
                                                                                                                                                                       cysteine
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disorders (Crohn's disease, anorexia, nausea, diarrhoea and jaundice); epithelial disorders (contact dermatitis, eczema, acne vulgaris, alopecia, scabies, insect bites and urticaria); reproductive disorder (infertility, disruption of estrous and menstrual cycle and gynaecomastia); and developmental disorders (renal tubular acidosis, Cushing's syndrome, seizure disorders, congenital glaucoma and cataract). PRTS DNA is also in useful is gene therapy. PRTS and its immunogenic fragments are useful for screening libraries of compounds in several drug
                                                                                                                                                                                                               include, cell proliferative disorders (arteriosclerosis, atherosclerosis, hepatitis, psoriasis and cancers); autoimmune/inflammatory disorders (AIDS, Addison's disease, allergy, anaemia, asthma, atopic dermatitis, diabetes mellitus, glomerulonephritis, multiple sclerosis, osteoporosis, trauma, Grave's disease, rheumatoid arthritis, ulcerative colitis, and viral, bacterial, fungal, parasitic, protozoal and helminthic infections); cardiovascular disorders (myocardial infarction, ischaemic heart disease and hypertension); neurological disorders (epilepsy, Alzhelmer's disease, Pitok's disease, Huntington's disease, dementia, parkinson's disease, stroke, mental disorders including mood, anxiety and seasonal affective disorder and prion diseases); gastrointestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-MAY-2000; 2000US-203566P
17-MAY-2000; 2000US-205803P
25-MAY-2000; 2000US-207477P
01-JUN-2000; 2000US-209402P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 121-123; 151pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human proteases and polynucleotides encoding the proteases, useful for treating, diagnosing or preventing cell proliferative, cardiovascular, autoimmune/inflammatory, neurological and developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to human proteases (PRTS1-14) and its corresponding CDNA molecules. Human PRTS and its nucleic acid molecule are useful for the diagnosis, treatment and prevention of disorders associated with increased or decreased expression of PRTS. Examples of such disorders
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Sequence
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OB, Gandhi A
                                     assays. The
703
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  AA;
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                                       present sequence is human protease
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MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , Patterson C, Walia NK,
Baughn MR, Azimzai Y,
Hernandez R, Policky JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Walia NK, Neuroni Y, Elliott
                                         PRTS-3
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                                       protein.
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                                                                                                                                                                                                                                                                    Similarity
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                              TALRKAGETLNSQVQQTIALRYACSKLGINFDSFVACMIRLETLFKLFSLLDEDKDGMVQ
                                              KALEEAGFKMPCQLHQVIVARFADDQLIIDFDNFVRCLVRLETLFKIFKQLDPENTGTIE
                                                                                    FDGFNINTCREMISLLDSNGTGTLGAVEFKTLWLKIQKYLEIYWETDYNHSGTIDAHEMR
                                                                                                             SDGFSIETCKIMVDMLDSDGSGKLGLKEFYILWTKIQKYQKIYREIDVDRSGTMNSYEMR
                                                                                                                                          LEIGDVVAGNPYEPHPSEVDQEDDQFRRLFEKLAGKDSEITANALKILLNEAFSKRTDIK
                                                                                                                                                                                                RDFFLAYQPSARTSTYVNLREVSGRARLPPGEYLVVPSTFEPFKDGEFCLRVFSEKKAQA
                                                                                                                                                                                                                                                       Conservative
    247
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52.4%; Pred. No. 9.90
Live 45; Mismatches
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                                                                                                                                                                                                                                                                                 Length
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LSLAEWLC

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RESULT 15
AAU72884
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                                  Qy
                                                                       Query Match
Best Local S
Matches 130
                                                                                                                                                                                              polypeptide (I) and polynucleotide (II) encoding (I). (I) may be used to screen for substances (S) that may modulate its activity. Administering S (which modulates protease activity in vitro) may be used to treat a disease or disorder selected from cancers (e.g., of tissues, of blood or haematopoletic origin, of the breast, colon, lung, prostrate, cervical, brain, ovarian, bladder or kidney), immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases (e.g., central or peripheral nervous system diseases, migraine, pain, sexual dysfunction, mood disorders, attention disorders, cognition disorders, hypotension, hypertension, psychotic disorders, neurological disorders and dyskinesias), metabolic disorders and inflammatory disorders such as those bowe. AAUTSAF6-AAUTS910 represent human protease among acid segmences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; protease; PCR primer; cytostatic; immunomodulator; cardiant; vasotropic; antimigraine; analgesic; endocrine; noctropic; tranquiliser; hypertensive; hypotensive; neuroleptic; neuroprotective; anabolic; anorectic; antiinflammatory; aspartyl protease; cysteine protease; metalloprotease; serine protease; cancer; haematopoletic; breast; colon; lung; prostrate; cervical; brain; ovarian; bladder; kidney; pain; immune-related disease; cardiovascular disease; neuronal disease; migraine; sexual dysfunction; mood disorder; attention disorder; cognition disorder; hypotension; hypertension; psychotic disorder; dyskinesia; metabolic disorder; inflammatory disorder.
                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated, enriched, or purified protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 28; Figure 2B; 232pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel protease polypeptide useful for screening for substances that may be used to treat, e.g., cancers, immune-related diseases, cardiovascular disease, migraine, pain, psychotic and inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-041502/05
N-PSDB; AAS97167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-MAY-2000; 2000US-201879P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SUGE-) SUGEN INC
 452
                                                                         al Similarity
130; Conserv
                   KNFFLTNRARERSDTFINLREVLNRFKLPPGEYILVPSTFEPNKDGDFCIRVFSEKKADY 60
RDFFLAYQPSARTSTYVNLREVSGRARLPPGEYLVVPSTFEPFKDGEFCLRVFSEKKAQA 511
                                                                                                                                                                                      amino
                                                                                                                                                  703
                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001WO-US14431
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                                                                                                                                                                                    acid
                                                                                                                                                                                    sequences of the invention.
                                                                                        51.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    partial protein sequence
                                                                     Score 668.5; DB 23;
Pred. No. 9.9e-59;
Pred. No. 9.9e-59;
                                                                                                           DB 23;
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                                                                         Indels
                                                                                                           Length 703;
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В
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692
                                     632 TALRKAGFTLNSQVQQTIALRYACSKLGINFDSFVACMIRLETLFKLFSLLDEDKDGMVQ
                                                                                             120
                 240 LDLISWLC 247
                                                                       KALEEAGFKMPCQLHQVIVARFADDQLIIDFDNFVRCLVRLETLFKIFKQLDPENTGTIE
                                                                                                               QAVDDEIEANLEEFDISE-DDIDDGFRRLFAQLAGEDAEISAFELQTILRRVLAKRQDIK 119
LSLAEWLC
699
                                      691
                                                                          631
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